

WEST**Freeform Search**

Database: **US Patents Full-Text Database** ▲
 JPO Abstracts Database
 EPO Abstracts Database
 Derwent World Patents Index
 IBM Technical Disclosure Bulletins ▼

Term: filter library ▲ ▼

Display: 10 Documents in Display Format: rev Starting with Number 1

Generate: ☐ Hit List ☒ Hit Count ☐ Image

Search

Clear

Help

Logout

Interrupt

Main Menu

Show S Numbers

Edit S Numbers

Preferences

Search History

Today's Date: 2/2/2001

<u>DB Name</u>	<u>Query</u>	<u>Hit Count</u>	<u>Set Name</u>
USPT	filter library	39	<u>L13</u>
USPT	110 and filter library	1	<u>L12</u> ✕
USPT	digital filter and ((435/4 or 436/\$)!ccls.)	16	<u>L11</u>
USPT	digital filter	8994	<u>L10</u>
USPT	(filter same (correction factor)) and ((435/\$ or 436/\$)!ccls.)	11	<u>L9</u>
USPT	17 and ((435/\$ or 436/\$)!ccls.)	19	<u>L8</u>
USPT	cluster same ((artifact) or (correction factor))	114	<u>L7</u>
USPT	15 not 12	3	<u>L6</u>
USPT	13 and (artifact and (correction factor))	4	<u>L5</u>
USPT	13 and (artifact and aberration)	1	<u>L4</u>
USPT	artifact and ((435/6)!CCLS.)	436	<u>L3</u>
USPT	11 and ((435/6)!CCLS.)	6	<u>L2</u>
USPT	(correction factor) same (assay)	54	<u>L1</u>

WEST

Generate Collection

Search Results - Record(s) 1 through 10 of 11 returned.☐ 1. Document ID: US 5770389 A

L9: Entry 1 of 11

File: USPT

Jun 23, 1998

US-PAT-NO: 5770389

DOCUMENT-IDENTIFIER: US 5770389 A

TITLE: Apparatus and method for determining the quantity of an analyte in a biological sample by means of transmission photometry

DATE-ISSUED: June 23, 1998

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Ching; Shan-Fun	Libertyville	IL	N/A	N/A
Hinger; Joanell Veronica	Arlington Heights	IL	N/A	N/A
Stimpson; Donald Irvine	Gurnee	IL	N/A	N/A
Gordon; Julian	Lake Bluff	IL	N/A	N/A

US-CL-CURRENT: 435/7.92; 250/214A, 250/214LS, 250/214RC, 250/214SW, 356/432, 356/433, 356/484, 377/12, 377/23, 377/53, 377/58, 422/56, 422/57, 422/82.05, 422/82.08, 435/287.1, 435/287.2, 435/287.7, 435/810, 436/514, 436/518, 436/506, 436/810

ABSTRACT:

A device and method for quantitative determination of an analyte in a biological sample utilizes a non-transparent support medium for retaining a chromatogenic reaction product with the medium being exposed to a source of light for transmitting therethrough a scattered, uniform response light signal which is collected at a photosensitive device whereby the amount of the analyte is correlated to the intensity of the response light signal. The response light signal may be converted to a time-duration signal proportional to light intensity to facilitate the quantitative determination.

38 Claims, 6 Drawing figures Exemplary Claim Number: 1
Number of Drawing Sheets: 3

Full	Title	Citation	Front	Review	Classification	Date	Reference	Claims	RMC	Draw Desc	Image
------	-------	----------	-------	--------	----------------	------	-----------	--------	-----	-----------	-------

☐ 2. Document ID: US 5573909 A

L9: Entry 2 of 11

File: USPT

Nov 12, 1996

US-PAT-NO: 5573909

DOCUMENT-IDENTIFIER: US 5573909 A

TITLE: Fluorescent labeling using microparticles with controllable stokes shift

DATE-ISSUED: November 12, 1996

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Singer; Victoria L.	Eugene	OR	N/A	U/A
Hangland; Richard P.	Eugene	OR	N/A	N/A

US-CL-CURRENT: 435/6; 435/5, 435/7.1, 436/172, 436/518, 436/523, 436/531,
436/532, 436/533, 436/534, 436/546, 436/805

ABSTRACT:

The invention relates to methods for labeling or detecting one or more target materials using surface coated fluorescent microparticles with unique characteristics. The unique microparticles used to practice the invention have at least two components: an external substance or coating that is selective for each target material and an internal mixture of multiple fluorescent dyes. The mixture of dyes is a series of two or more fluorescent dyes having overlapping excitation and emission spectra allowing efficient energy transfer from the excitation wavelength of the first dye in the series, transfer through the dyes in the series and re-emitted as an optical signal at the emission wavelength of last dye in the series, resulting in a desired effective Stokes shift for the microparticle that is controlled through selection of appropriate dyes. The unique microparticles are combined with a sample thought to contain the target material(s), so that the microparticles label the target materials. The sample is then optionally illuminated, resulting in fluorescence of the microparticles that is used to detect one or more target materials.

30 Claims, 11 Drawing figures Exemplary Claim Number: 1

Number of Drawing Sheets: 6

Full	Title	Citation	Front	Review	Classification	Date	Reference	Claims	KWC	Draw Desc	Image
------	-------	----------	-------	--------	----------------	------	-----------	--------	-----	-----------	-------

☐ 3. Document ID: US 5326692 A

L9: Entry 3 of 11

File: USPT

Jul 5, 1994

US-PAT-NO: 5326692

DOCUMENT-IDENTIFIER: US 5326692 A

TITLE: Fluorescent microparticles with controllable enhanced stokes shift

DATE-ISSUED: July 5, 1994

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Brinkley; John M.	Elmira	OR	N/A	N/A
Haugland; Richard P.	Eugene	OR	N/A	N/A
Singer; Victoria L.	Eugene	OR	N/A	N/A

US-CL-CURRENT: 435/6, 252/301.34, 252/301.35, 428/402, 435/7.92, 436/518,
436/523, 436/529, 436/531, 436/546, 436/801

ABSTRACT:

The invention relates to microparticles incorporating a series of two or more fluorescent dyes having overlapping excitation and emission spectra allowing efficient energy transfer from the excitation wavelength of the first dye in the series, transfer through the dyes in the series and re-emitted as an optical signal at the emission wavelength of last dye in the series, resulting in a desired effective Stokes shift which is controlled through selection of appropriate dyes.

15 Claims, 4 Drawing figures Exemplary Claim Number: 1
Number of Drawing Sheets: 3

Full	Title	Citation	Front	Review	Classification	Date	Reference	Claims	KWIC	Draw Desc	Image
------	-------	----------	-------	--------	----------------	------	-----------	--------	------	-----------	-------

☐ 4. Document ID: US 4918004 A

L9: Entry 4 of 11

File: USPT

Apr 17, 1990

US-PAT-NO: 4918004
DOCUMENT-IDENTIFIER: US 4918004 A

TITLE: Method of calibrating a flow cytometer or fluorescence microscope for quantitating binding antibodies on a selected sample, and microbead calibration kit therefor

LATE-ISSUED: April 17, 1990

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Schwartz; Abraham	Durham	NC	N/A	N/A

US-CL-CURRENT: 435/7.24, 435/29, 435/34, 435/5, 435/7.21, 435/7.25, 435/810, 435/974, 436/10, 436/510, 436/512, 436/533, 436/534, 436/543, 436/800, 436/811

ABSTRACT:

A method for calibrating a flow cytometer or fluorescence microscope in terms of number of binding antibodies as a function of fluorescence intensity value measured on the flow cytometer or fluorescence microscope, and subsequent measuring of a sample to which the antibodies are bindable. Also disclosed is a microbead calibration kit for carrying out the calibration method of the invention. The disclosed calibration methodology provides a direct relationship between instrument response and numbers of binding antibodies, independent of the fluorochrome employed to label the samples being measured. The method has utility in monitoring the status of an antigenic cellular condition in which the number of antibodies binding to successively obtained cellular samples is determined, to establish the progressionary character of the antigenic cellular condition, in a host from which the cellular samples are taken.

19 Claims, 1 Drawing figures Exemplary Claim Number: 7
Number of Drawing Sheets: 1

Full	Title	Citation	Front	Review	Classification	Date	Reference	Claims	KWIC	Draw Desc	Image
------	-------	----------	-------	--------	----------------	------	-----------	--------	------	-----------	-------

☐ 5. Document ID: US 4528131 A

L9: Entry 5 of 11

File: USPT

Jul 9, 1985

US-PAT-NO: 4528131
DOCUMENT-IDENTIFIER: US 4528131 A

TITLE: Process and preparation for the quantitative determination of substances able to bind to cerebral receptors and a process for preparing the preparation

DATE ISSUED: July 9, 1985

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Kardos; Julianna	Budapest	N/A	N/A	HUN
Maksay; Gabor	Budapest	N/A	N/A	HUN
Simonyi; Miklos	Budapest	N/A	N/A	HUN

US-CL-CURRENT: 424/570, 436/503, 436/504, 436/545, 436/547, 436/804, 436/815

ABSTRACT:

A process for preparing a stable receptor preparation suitable for the quantitative determination of substances able to bind to cerebral receptors in which a brain or brain-region material is homogenized with an aqueous solution of an inert substance soluble in water; the formed homogenizate is centrifuged at an acceleration of 800 to 1100 g for 8 to 20 minutes to form a supernatant; the brain or brain-region material is isolated from the supernatant by centrifuging the supernatant at an acceleration of 18,000 to 22,000 g for 10 to 20 minutes, the thus-obtained solid substance is rehomogenized in distilled water; the homogenizate is frozen and then thawed and thereafter centrifuged at an acceleration of 7000 to 9000 g for 5-15 minutes; the supernatant is isolated, centrifuged at an acceleration of 35,000 to 45,000 g for 20 to 30 minutes; the obtained solid substance is washed with an aqueous buffer solution of a pH value between 6 and 8, and a suspension consisting of the solid substance and the washing liquid is frozen and then thawed at least once and thereafter the suspension is lyophilized.

8 Claims, 0 Drawing figures Exemplary Claim Number: 1

Full	Title	Citation	Front	Review	Classification	Date	Reference	Claims	KWMC	Draw Desc	Image
------	-------	----------	-------	--------	----------------	------	-----------	--------	------	-----------	-------

6. Document ID: US RE30627 E

L9: Entry 6 of 11

File: USPT

May 26, 1981

US-PAT-NO: PE30627
DOCUMENT-IDENTIFIER: US RE30627 E

TITLE: Apparatus for performing chemical and biological analysis

DATE-ISSUED: May 26, 1981

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Bagshawe; Kenneth D.	London	N/A	N/A	GBL
Kemle; James E.	Burgess Hill	N/A	N/A	GB2

US-CL-CURRENT: 436/48, 218/387, 422/101, 422/63, 422/66, 422/71, 436/44,
436/57, 436/808

ABSTRACT:

A system for the automated analysis of large numbers of liquid samples, in which a multiplicity of sample tubes are loaded in racks into a cassette and the loaded cassette is transferred from station to station, with operations of sample insertion, dilution, reagent addition and withdrawal for filtering being performed at successive stations. At each station there is a separate processing module adapted to receive the cassette, each module including the apparatus necessary for performing one of the abovementioned operations on each individual sample tube when it is located at a particular operational location in the cassette. Each module also has members for shifting the racks in the cassette in such manner that all tubes pass through the operational location in turn while strictly maintaining the same order of sequence throughout the operations.

54 Claims, 4 Drawing figures Exemplary Claim Number: 10
Number of Drawing Sheets: 3

Full	Title	Citation	Front	Review	Classification	Date	Reference	Claims	KVMC	Draw Desc	Image
------	-------	----------	-------	--------	----------------	------	-----------	--------	------	-----------	-------

☐ 7. Document ID: US 4038150 A

L9: Entry 7 of 11

File: USPT

Jul 26, 1977

US-PAT-NO: 4038150

DOCUMENT IDENTIFIER: US 4038150 A

TITLE: Sample mixing and centrifugation apparatus

DATE-ISSUED: July 26, 1977

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Eorn; Gordon L.	Dallas	TX	N/A	N/A
Hill; Joseph M.	Dallas	TX	N/A	N/A

US-CL-CURRENT: 435/288.2; 435/30, 604/415

ABSTRACT:

An apparatus for mixing fluids especially suitable for use in laboratory tests for the detection of microbial pathogens which includes an elongated centrifugation vessel, an injectable closure, completely enclosing a treating fluid chamber, and a novel stylus which causes a sample to be admixed and commingled with a treating fluid upon injection. The treating fluid is disposed within the treating fluid chamber and a sterile aqueous solution having a greater density than a sample fluid but able to selectively receive microbial pathogens from the sample fluid is disposed within an evacuated space within the centrifugation vessel. The sample is mixed with the treating fluid when the novel stylus is injected through the injectable closure means facilitating contact of the treating fluid and the sample via an aperture or apertures longitudinally spaced along the stylus so as to be within the treating fluid chamber upon injection of the stylus. The sample-treating fluid mixture then continues its flow through the canalis of the stylus and is deposited on the aqueous solution within the evacuated space of the centrifugation vessel.

53 Claims, 11 Drawing figures Exemplary Claim Number: 1
Number of Drawing Sheets: 1

Full	Title	Citation	Front	Review	Classification	Date	Reference	Claims	KMC	Draw Desc	Image
------	-------	----------	-------	--------	----------------	------	-----------	--------	-----	-----------	-------

☐ 8. Document ID: US 3932222 A

L9: Entry 8 of 11

File: USPT

Jan 13, 1976

US-PAT-NO: 3932222
DOCUMENT-IDENTIFIER: US 3932222 A

TITLE: For isolating pathogenic microorganisms

DATE ISSUED: January 13, 1976

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Born; Gordon L.	Dallas	TX	N/A	N/A

US-CI-SUPPLEMENT: 435/288.1; 422/913, 435/30, 435/34, 604/416

ABSTRACT:

A mixing and centrifugation device particularly suitable for use in procedures involving detection of microbial pathogens which includes an elongated enclosed centrifugation receptacle containing an evacuated space and having an injectable closure on an end thereof with an enclosed treating fluid chamber disposed in communication and adjacent the injectable closure and separated from the evacuated space by a thin rupturable membrane. A sample treating fluid is carried within the enclosed treating fluid chamber and a sterile aqueous solution having a greater density than a sample fluid but able to selectively receive microbial pathogens from the sample fluid is disposed within the evacuated chamber. A sample is deposited on the sterile aqueous solution via an injection needle by passing the injection needle through the injectable closure, the enclosed treating fluid chamber, and rupturing the thin membrane such that the sample treating fluid contacts the sample as it passes from the injection needle and is deposited on the liquid filter medium.

24 Claims, 8 Drawing figures Exemplary Claim Number: 1
Number of Drawing Sheets: 1

Full	Title	Citation	Front	Review	Classification	Date	Reference	Claims	KMC	Draw Desc	Image
------	-------	----------	-------	--------	----------------	------	-----------	--------	-----	-----------	-------

☐ 9. Document ID: US 3928139 A

L9: Entry 9 of 11

File: USPT

Dec 23, 1975

US-PAT-NO: 3929139

DOCUMENT-IDENTIFIER: US 3929139 A

TITLE: Detection of microbial pathogens

DATE-ISSUED: December 23, 1975

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Dorn; Gordon L.	Dallas	TX	N/A	N/A

US-CL-CURRENT: 435/34, 435/30, 435/308.1, 435/36, 435/38, 435/39, 435/322,
435/343, 435/352, 435/373, 435/375, 435/383, 435/385, 435/921, 435/921

ABSTRACT:

A method and apparatus are disclosed which provide for the rapid quantitative detection of microbial pathogens in a sample fluid such as blood. Initially the pathogens are concentrated by depositing the sample fluid on a liquid filter medium such as a concentrated aqueous solution of sucrose or a microporous aqueous solution of a crosslinked polymer having a greater density than the sample, and microporous openings throughout its solubilized network (which range in size between about 1 micron and about 7 microns) and then the material is subjected to centrifugation to cause the pathogens in the sample to selectively pass into the liquid filter medium. This step not only concentrates the pathogens but also separates them from the other components of the sample such as antimicrobial constituents of blood and medicants present in blood samples, such as antibiotics. The liquid filter medium containing the concentrated pathogens is then added to nutrient media for culturing and quantitative counting.

47 Claims, 10 Drawing figures Exemplary Claim Number: 1
Number of Drawing Sheets: 1

Full	Title	Citation	Front	Review	Classification	Date	Reference	Claims	KWIC	Draw. Desc	Image
------	-------	----------	-------	--------	----------------	------	-----------	--------	------	------------	-------

☐ 10. Document ID: US 3875012 A

L9: Entry 10 of 11

File: USPT

Apr 1, 1975

US-PAT NO: 3875012

DOCUMENT-IDENTIFIER: US 3875012 A

TITLE: Apparatus and method for the detection of microbial pathogens

DATE-ISSUED: April 1, 1979

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Lorn; Gordon L.	Dallas	TX	N/A	N/A
Hill; Joseph M.	Dallas	TX	N/A	N/A

US-CL-CURRENT: 435/243, 205/222, 215/247, 215/DIG.3, 422/913, 435/30,
435/309.1, 435/309.2, 435/31, 435/39, 504/415

ABSTRACT:

An apparatus for the isolation and concentration of microbial pathogens from a sample fluid which comprises an elongated enclosed centrifugation receptacle containing an evacuated space in contact with a sterile aqueous solution of a material having a greater density than the sample fluid but able to selectively receive microbial pathogens from the sample fluid, a first injectable closure on one end thereof and a second injectable closure on its other end, and a sterile end chamber in communication with the second injectable closure which contains a sample fluid treating solution together with an injection needle assembly which when actuated will pass through the second injectable closure means and allow communication between the chamber and the evacuated space within the centrifugation receptacle to thereby allow the treating fluid to flow from the chamber into the evacuated space. Thereafter, the sample fluid can be injected into the evacuated chamber of the centrifugation tube through a needle passing through the first injectable closure and allow the sample fluid to admix with the pretreating solution in the evacuated chamber. The article is then subjected to centrifugation to allow the microbial pathogens to selectively pass into the liquid filter medium.

25 Claims, 6 Drawing figures Exemplary Claim Number: 15
Number of Drawing Sheets: 1

Full	Title	Citation	Front	Review	Classification	Date	Reference	Claims	KWIC	Draw Desc	Image
------	-------	----------	-------	--------	----------------	------	-----------	--------	------	-----------	-------

[Generate Collection](#)

Terms	Documents
(filter same (correction factor)) and ((435/\$ or 436/\$)! ccls.)	11

[Display](#)[10](#)Documents, starting with Document: [11](#)[Display Format:](#)[REV](#)[Change Format](#)

WEST[Generate Collection](#)**Search Results - Record(s) 11 through 11 of 11 returned.**☐ 11. Document ID: US 3825410 A

Ln: Entry 11 of 11

File: USFT

Jul 23, 1974

US-PAT-NO: 3825410

DOCUMENT-IDENTIFIER: US 3825410 A

TITLE: PERFORMANCE OF ROUTINE CHEMICAL REACTIONS IN COMPARTMENTALIZED CONTAINERS

DATE-ISSUED: July 23, 1974

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Bagshawe; Kenneth Dawson	London W 1	N/A	N/A	EN

US-CL-CURRENT: 436/57; 206/459.1, 206/509, 421/101, 422/102, 422/61, 422/66, 422/67, 422/71

ABSTRACT:

In the performance of routine chemical and/or biological reactions, such as saturation analysis using a radioactive marker substance, the standard reactants are dispensed in appropriate amounts, in a prior operation, into a compartmentalized storage container which also constitutes the reaction vessel, the reactants being maintained in a stable unreactive state, such as by freeze drying, until the analysis is to be performed. The reaction is initiated by introduction of a sample to be analysed, whereafter separation of bound and free ligand can be performed either within the compartmentalized vessel itself or externally.

25 Claims, 13 Drawing figures Number of Drawing Sheets: 5

Full	Title	Citation	Front	Review	Classification	Date	Reference	Claims	KMIC	Draw Desc	Image
------	-------	----------	-------	--------	----------------	------	-----------	--------	------	-----------	-------

[Generate Collection](#)

Terms	Documents
(filter same (correction factor)) and ((435/\$ or 436/\$) ccls.)	11

[Display](#)[10](#)Documents, starting with Document: [11](#)**Display Format:**[FEV](#)[Change Format](#)

WEST

Generate Collection

Search Results - Record(s) 1 through 3 of 3 returned.☐ 1. Document ID: US 6150089 A

L6: Entry 1 of 3

File: USPT

Nov 21, 2000

US-PAT-NO: 6150089

DOCUMENT-IDENTIFIER: US 6150089 A

TITLE: Method and characterizing polymer molecules or the like

DATE-ISSUED: November 21, 2000

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Schwartz; David	New York	NY	N/A	N/A

US-CL-CURRENT: 435/6; 204/450, 204/456, 204/600, 204/606

ABSTRACT:

A method for observing and determining the size of individual molecules and for determining the weight distribution of a sample containing molecules of varying size, which involves placing a deformable or nondeformable molecule in a medium, subjecting the molecule to an external force, thereby causing conformational and/or positional changes, and then measuring these changes. Preferred ways to measure conformational and positional changes include: (1) determining the rate at which a deformable molecule returns to a relaxed state after termination of the external force, (2) determining the rate at which a molecule becomes oriented in a new direction when the direction of the perturbing force is changed, (3) determining the rate at which a molecule rotates, (4) measuring the length of a molecule, particularly when it is at least partially stretched, or (5) measuring at least one diameter of a spherical or ellipsoidal molecule. Measurements of relaxation, reorientation, and rotation rates, as well as length and diameter can be made using a light microscope connected to an image processor. Molecule relaxation, reorientation and rotation also can be determined using a microscope combined with a spectroscopic device. The invention is particularly useful for measuring polymer molecules, such as nucleic acids, and can be used to determine the size and map location of restriction digests. Breakage of large polymer molecules mounted on a microscope slide is prevented by condensing the molecules before mounting and unfolding the molecules after they have been placed in a matrix.

16 Claims, 53 Drawing figures Exemplary Claim Number: 1,11

Number of Drawing Sheets: 16

Full	Title	Citation	Front	Review	Classification	Date	Reference	Claims	KWIC	Draw Desc	Image
------	-------	----------	-------	--------	----------------	------	-----------	--------	------	-----------	-------

☐ 2. Document ID: US 6027884 A

L6: Entry 2 of 3

File: USPT

Feb 22, 2000

US-PAT-NO: 6027884
DOCUMENT-IDENTIFIER: US 6027884 A

TITLE: Thermodynamics, design, and use of nucleic acid sequences

DATE-ISSUED: February 22, 2000

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Lane; Michael J.	Baldwinsville	NY	N/A	N/A
Benight; Albert S.	Schaumburg	IL	N/A	N/A
Faldasz; Brian D.	Maynard	MA	N/A	N/A

US-CL-CURRENT: 435/6; 435/5, 536/24.2, 536/24.33

ABSTRACT:

A method of providing the sequence of a single stranded nucleic acid molecule, which, when hybridized to a complementary single stranded molecule, results in a double stranded (duplex) structure having a preselected value for a free energy parameter.

6 Claims, 25 Drawing figures Exemplary Claim Number: 1
Number of Drawing Sheets: 11

Full	Title	Citation	Front	Review	Classification	Date	Reference	Claims	KWIC	Draw Desc	Image
------	-------	----------	-------	--------	----------------	------	-----------	--------	------	-----------	-------

☐ 3 Document ID: US 5654147 A

LG: Entry 3 of 3

File: USPT

Aug 5, 1997

US-PAT-NO: 5654147
DOCUMENT-IDENTIFIER: US 5654147 A

TITLE: Method of hybridization using oligonucleotide probes

DATE-ISSUED: August 5, 1997

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Wood; William L.	San Mateo	CA	N/A	N/A
Lasky; Laurence A.	Sausalito	CA	N/A	N/A

US-CL-CURRENT: 435/6; 435/5, 435/51.2, 536/24.3, 536/24.32, 536/24.33

ABSTRACT:

An improved method of hybridization with oligonucleotide probes using tetramethylammonium chloride is provided. The method is useful for screening mixtures of DNA sequences, including libraries of high DNA sequence complexity, with a single oligonucleotide probe or a pool of probes representing all possible codon choices for a short amino acid sequence.

5 Claims, 41 Drawing figures Exemplary Claim Number: 1
Number of Drawing Sheets: 32

Full	Title	Citation	Front	Review	Classification	Date	Reference	Claims	KWIC	Draw. Desc	Image
------	-------	----------	-------	--------	----------------	------	-----------	--------	------	------------	-------

Generate Collection

Terms	Documents
15 not 12	3

Display

10

Documents, starting with Document:

3

Display Format:

rev

Change Format

WEST☐ Generate Collection

LG: Entry 1 of 3

File: USPT

Nov 21, 2000

DOCUMENT-IDENTIFIER: US 6150089 A

TITLE: Method and characterizing polymer molecules or the like

DEPR:

High image quality greatly facilitates image processing. Fluorescence images of DNAs obtained in fluid rather than gel are brighter, sharper and relatively free of fluorescing artifacts. Consequently, they are ideal for unattended image processing since they can be transformed into reliable binary or digital images, which are easily accepted by our processing algorithms. This high throughput sizing methodology can be tested and benchmarked by using a series of Not I digested yeast chromosomes mixtures (containing DNAs 30-900 kb), of increasing complexity. Statistical analysis to calculate the precision of single measurements can be performed and the ultimate accuracy of this methodology determined. Confidence intervals are determined to establish the minimum number of molecules necessary for adequate analysis of complex mixtures. This analysis will help determine the usable size resolution and size discrimination levels. Sources of noise and systematic error are detected and eliminated as much as possible. A lower size limit of 5-20 kb and an increased upper size limit are provided by the present invention since molecules with contour lengths greater than the microscope viewing field are sized by offsetting a known distance from the interface and monitoring only still ends.

DEPR:

The gel-fluid interface system can be used in this invention to obtain high resolution fluorescence intensity measurements of single molecules. Measurement precision can be increased and lower size limitations made for these measurements. Increased sizing performance accrues from a number of factors, such as, but not limited to, the simultaneous use of three sizing methods will increase precision and accuracy (length, relaxation and intensity); the fluid-gel interface system produces optically flat molecules more consistently than gel fixation; the degree of molecular elongation is more controllable than gel fixation, and the elimination of gel provides sharper, brighter images that are more free of fluorescing artifacts. As mentioned previously, high quality images are easier to image process automatically.

DEPR:

To minimize errors arising from relative intensity measurements, a number of internal standards can be placed into samples so that fluorescence non-linearities arising from uneven illumination can be substantially reduced or eliminated. The internal standard preferably meets several requirements: 1) negatively charged to avoid sticking to DNA; 2) fluorescent in the same absorption and emission wavelengths as the DNA-fluorochrome complex, and 3) readily distinguishable from the test DNA molecules to be measured. Small DNA molecules (20-50 kb) can be used as internal standards. These molecules are dispersed throughout the sample to be measured and preferably react identically as the sample DNA to illumination and electrophoretic conditions (e.g., in free solution). The internal standards to determine relative mass, instead of using contiguous restriction digestion products from the same parental molecule. To optimize these determinations, we will systematically vary the DNAs used as standards, utilizing standards of different sizes, and measure their relative fluorescence intensities. If necessary, empirical

correction factors are calculated to ensure linearity.

LEPP:

Optical Mapping of Large Mammalian Genomes: Ferrin and Camerini-Otero (68) have shown that two RARE sites can be designed to selectively cleave a sizable mammalian genomic stretch; it can then be resolved on a pulsed field gel from about genomic DNA. These authors, as well as Hoch and Szybalski (67), suggested that these dissected and isolated genomic sections could be used to construct locus-specific libraries for physical mapping studies. These libraries help in tying contigs together or in mapping uncloneable regions, for example. Although directly mapping the small amount of cleaved, genomic DNA obtained from gels would be convenient, obviating steps and artifacts of cloning, the concentration of the recovered DNA is generally insufficient for direct analysis, except by PCR and optical mapping.

LEPP:

Influence of coil relaxation on detection of cuts. Aside from cases involving small fragments, incomplete digestion is seen in all the histograms in FIG. 7. While potential cases range from photo irradiation artifacts to interactions imposed by the current design of the microscope chamber, partial digestion observed here is attributable mostly to incomplete coil relaxation at a given cut site, due to relaxation modes that fail to produce a gap or distinct ball. A variety of different relaxation modes are observed in actual practice, some of which are sketched in FIG. 8. Relaxation modes can both facilitate (8-D) and hinder cut detection (8-H). Application of electric or flow fields might be used to trigger relaxation at such sites and permit their detection. Parallel electrophoresis experiments show essentially complete digestion under similar experimental conditions (Hernandez).

COOP:

435/6

WEST

Generate Collection

Search Results - Record(s) 1 through 6 of 6 returned.☐ 1. Document ID: US 6143502 A

L2: Entry 1 of 6

File: USPT

Nov 7, 2000

US-PAT-NO: 6143502

DOCUMENT-IDENTIFIER: US 6143502 A

TITLE: Dual-luciferase reporter system

DATE-ISSUED: November 7, 2000

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Greutsmann; Guido	Salt Lake City	UT	N/A	N/A
Gesteland; Raymond F.	Salt Lake City	UT	N/A	N/A
Atkins; John F.	Verrieres le Buisson	N/A	N/A	FRX

US-CL-CURRENT: 435/6; 435/320.1, 435/8

ABSTRACT:

Plasmids and methods of use for assaying translational recoding are disclosed. The plasmids contain a constitutively expressed renilla (*Renilla reniformis*; sea pansy) luciferase gene, a polylinker for insertion of a selected DNA segment, and an out-of-frame firefly luciferase gene. Recoding is determined by monitoring luminescence of the firefly luciferase normalized to the luminescence of the renilla luciferase.

26 Claims, 4 Drawing figures Exemplary Claim Number: 1
Number of Drawing Sheets: 2

Full	Title	Citation	Front	Review	Classification	Date	Reference	Claims	KWIC	Draw Desc	Image
------	-------	----------	-------	--------	----------------	------	-----------	--------	------	-----------	-------

☐ 2. Document ID: US 6110671 A

L2: Entry 2 of 6

File: USPT

Aug 29, 2000

US PAT-NO: 611 671
DOCUMENT-IDENTIFIER: US 611-671 A

TITLE: Method of measuring tumor suppressor gene p53

DATE-ISSUED: August 29, 2000

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Kim; Jerome H.	Baltimore	MD	N/A	N/A

US-CL-CURRENT: 435/6; 435/91.2, 536/23.1, 536/24.3, 536/24.32, 536/24.33

ABSTRACT:

The instant invention provides a means for quantitatively determining the vel of tumor suppressor gene p53 by determination of level of messenger ribonucleic acid (mRNA) of the gene in a sample when compared with a prepared standard. The assay is quantitative in that the specific number of copies of the p53 mRNA in a sample may be derived from a curve from a standard of p53 RNA. The RNA used in preparation of a standard curve to quantitate RNA is generated using a plasmid which is part of the invention. In the assay, the RNA is produced by a protein (RNA polymerase) that reads the DNA message and manufactures an RNA copy. The RNA content of the transcribed sample is determined spectrophotometrically to measure the molar concentration. With prior knowledge of the molecular weight of the transcribed RNA and using Avogadro's number, the actual number of molecules of transcribed "control" p53 RNA can be determined

4 Claims, 0 Drawing figures Exemplary Claim Number: 1

Full	Title	Citation	Front	Review	Classification	Date	Reference	Claims	KWIC	Draw Desc	Image
------	-------	----------	-------	--------	----------------	------	-----------	--------	------	-----------	-------

☐ 3. Document ID: US 5677133 A

L2: Entry 3 of 6

File: USPT

Oct 14, 1997

US-PAT-NO: 5677133
DOCUMENT-IDENTIFIER: US 5677133 A

TITLE: Dry chemistry cascade immunoassay and affinity assay

DATE-ISSUED: October 14, 1997

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Oberhardt, Bruce L.	Raleigh	NC	N/A	N/A

US-CL-CURRENT: 435/7.1, 422/57, 422/58, 422/61, 422/73, 435/13, 435/288.5,
435/288.7, 435/5, 435/6, 435/7.2, 435/7.4, 435/7.7, 435/7.92, 435/7.93,
435/7.94, 435/810, 436/46, 436/526, 436/527, 436/805, 436/806, 436/807,
436/808, 436/809, 436/810

ABSTRACT:

A method is described for performing an affinity assay comprising contacting a sample to be assayed for the presence of an analyte with a dry reagent containing the analyte (hapten, antigen, antibody, receptor, or complementary polynucleotide) bound to a reaction cascade initiator, an antibody or other binding pair partner reactive with said analyte, and magnetic particles, to form an assay mixture in a reaction chamber, incubating the assay mixture, applying an oscillating or moving static magnetic field to the assay mixture, activating the reaction cascade initiator to initiate a reaction cascade, monitoring the response of the magnetic particles to the oscillating or moving static magnetic field to provide a time varying signal, and determining the analyte concentration of the sample by analysis of the time varying signal, as well as a kit for performing the assay and a diagnostic system for performing the assay.

4 Claims, 20 Drawing figures Exemplary Claim Number: 1
Number of Drawing Sheets: 10

Full	Title	Citation	Front	Review	Classification	Date	Reference	Claims	KWIC	Draw Desc	Image
------	-------	----------	-------	--------	----------------	------	-----------	--------	------	-----------	-------

☐ 4. Document ID: US 5601991 A

L2: Entry 4 of 6

File: USPT

Feb 11, 1997

US-PAT-NO: 5225332

DOCUMENT-IDENTIFIER: US 5225332 A

TITLE: Process for manipulation of non-aqueous surrounded microdroplets

DATE ISSUED: July 6, 1993

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Weaver; James C.	Sudbury	MA	N/A	N/A
Joseph; Julian	Cedarhurst	NY	N/A	N/A

US-CL-CURRENT: 435/29, 428/402.2, 435/177, 435/192, 435/243, 435/30, 435/34,
435/5, 425/6, 425/7.1, 436/526, 436/535, 436/829

ABSTRACT:

A process for manipulation of liquid microdroplets is disclosed. The process involves formation of microdroplets such that physical forces based on particular interactions of the microdroplets with a surrounding non-aqueous fluid results can be used to alter the position of the microdroplets.

7 Claims, 0 Drawing figures Exemplary Claim Number: 1,4,5

Full	Title	Citation	Front	Review	Classification	Date	Reference	Claims	KWIC	Draw Desc	Image
------	-------	----------	-------	--------	----------------	------	-----------	--------	------	-----------	-------

☐ 6. Document ID: US 4959301 A

L2: Entry 6 of 6

File: USPT

Sep 25, 1990

US PAT-NO: 4959301
DOCUMENT-IDENTIFIER: US 4959301 A

TITLE: Process for rapidly enumerating viable entities

DATE-ISSUED: September 25, 1990

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Weaver; James C.	Sudbury	MA	N/A	N/A
Bliss; Jonathan G.	Somerville	MA	N/A	N/A
Williams; Gregory B.	Tewksbury	MA	N/A	N/A
Powell; Kevin T.	Boston	MA	N/A	N/A
Harrison; Gail I.	Watertown	MA	N/A	N/A

US-CL-CURRENT: 435/5, 435/177, 435/182, 435/29, 435/30, 435/32, 435/39, 435/6

ABSTRACT:

A process for rapidly enumerating viable biological entities is disclosed, wherein viability is determined by the criterion of growth of biological entities contained in microdroplets. Alternatively, in some cases, viability is determined by use of vital staining of biological entities contained in microdroplets. The process involves formation of microdroplets, which are very small volume liquid or gel particles, such that some of the microdroplets contain biological entities, followed by measurements of biological entities and of microdroplet volumes, such that use of statistical analysis can be used self-consistently to determine the number of viable entities per volume of a sample.

12 Claims, 0 Drawing figures Exemplary Claim Number: 1

Full	Title	Citation	Front	Review	Classification	Date	Reference	Claims	KWC	Draw Desc	Image
------	-------	----------	-------	--------	----------------	------	-----------	--------	-----	-----------	-------

Generate Collection

Terms	Documents
11 and ((435/6)!.CCLS.)	6

Display

10

Documents, starting with Document:

6

Display Format:

rev

Change Format

Generate Collection

Nov 7, 2000

The dual-luciferase assay is designed such that synthesis of the second reporter (firefly luciferase) is dependent on recoding. On its own, however, the amount of this reporter is not a direct reflection of the efficiency of recoding. In the absence of in-frame stop codons, a significant proportion of translating ribosomes disengage prematurely from the mRNA; this is often known as ribosome drop off. Early results from several laboratories have shown that 50 or more of *Escherichia coli* ribosomes drop off during synthesis of .beta.-galactosidase (J. L. Manley, Synthesis and Degradation of Termination and Premature-Termination Fragments of .beta.-Galactosidase In Vitro and In Vivo, 128 J. Mol. Biol. 407-432 (1978)); P. G. Kurland et al., Limitations of Translational Accuracy, in F. C. Neidhardt et al., *Escherichia coli* and *Salmonella typhimurium*. Cellular and Molecular Biology 979-1004 (2.sup.nd ed. 1996)). Ribosomes that drop off while decoding the firefly reporter will lead to an underestimate of the proportion of ribosomes that respond to the recoding signals unless a correction is made. The basis for a correction factor is the assumption that drop off during synthesis of the firefly reporter is proportional to completion of synthesis of this reporter. The correction factor is provided by a control in which all ribosomes that complete synthesis of the first reporter (renilla luciferase) continue translation by starting synthesis of the firefly luciferase reporter.

2101854 PM

WEST

Generate Collection

L2: Entry 2 of 6

File: USPT

Aug 29, 2000

DOCUMENT-IDENTIFIER: US 6110671 A

TITLE: Method of measuring tumor suppressor gene p53

BSPP:

The .beta.-actin curves are used to standardize the p53 copy number. For example, the p53 assay is performed using 2000 "cell equivalents of RNA determined from the number of cells counted by means such as hemocytometer. The p53 number control curve is calculated as used to estimate the number of copies of p53 found in a sample of 2000 cells. The separate RT-PCR for .beta.-actin can be performed on 500 cell equivalents of RNA from the sample and then compared to the data obtained from a serial dilution (100 cell equivalents to 1 cell equivalent) of RNA from a control PBMC sample. From this comparison a correction factor is obtained. For example, the .beta.-actin data may suggest that there is only 100 cell equivalents of RNA in the sample tested rather than the 500 cell equivalents expected under the circumstances. The p53 copy number of that sample is multiplied by a factor of 5 to correct for the "deficiency" in cell number.

DOOR:

435/6

WEST☐ Generate Collection

L2: Entry 3 of 6

File: USPT

Oct 14, 1997

DOCUMENT-IDENTIFIER: US 5677193 A

TITLE: Dry chemistry cascade immunoassay and affinity assay

DEPR:

To perform the quinidine assay, the reaction slide is placed in the instrument and automatically brought to operating temperature, typically 37.degree. C. for this assay system. A drop of blood is added to the reaction slide and sample well. The blood enters and dissolves the reagent. The magnetic particles are driven into motion by application of an oscillating magnetic field creating convection and mixing the reactants. During this period the anti-quinidine antibody is allowed to bind to the quinidine on the X.sub.a mutant-quinidine conjugate and to quinidine that may be present in the sample. This distribution of the fixed amount of antibody between conjugate and sample quinidine occurs as the reaction is allowed to continue during a predetermined incubation period. At the end of this incubation period, the temperature set point is rapidly increased by 8.degree. C./min to a level at which the X.sub.a mutant undergoes a conformational change and becomes active. At this point, the X.sub.a enzyme begins to convert prothrombin to thrombin at a rate proportional to the concentration of active X.sub.a enzyme. The X.sub.a enzyme sterically inactivated by antibody does not convert prothrombin to thrombin or converts it at an extremely low or negligible rate. Therefore, the concentration of X.sub.a -quinidine conjugate that has not reacted with antibody determines the rate of conversion of prothrombin to thrombin. The generated thrombin converts fibrinogen to fibrin, thus amplifying the chemical signal further. When fibrin formation reaches a critical stage, the clot or endpoint is detected by changes in the magnetic particle movement. The elapsed time from thermal triggering to clot endpoint is the clotting time. The clotting time is thus proportional to the quinidine in the sample. The actual quinidine concentration in the sample can be read automatically from a standard curve stored in the measuring instrument for that particular lot of reaction slides. This value can be converted to a plasma quinidine concentration, if desired, by correcting for the fraction of the reaction volume occupied by blood cells. A correction factor for total cell volume, in blood typically equivalent to hematocrit, may be entered into the instruments computer memory or this conversion may be performed from a sample chart.

DOXR:

4:5/6

WEST**End of Result Set**

Generate Collection

LN: Entry 6 of 6

File: USPT

Sep 25, 1990

DOCUMENT-IDENTIFIER: US 4959301 A

TITLE: Process for rapidly enumerating viable entities

DEPL:

which is the intermediate of the assay, thereby being the number of analyte entities per volume in the diluted sample. It is straightforward to then compute a correction factor, .function..sub.D, ##EQU16## for the dilution during the MD creation process, and thereby, to obtain the concentration, .rho..sub.analyte, of analyte entity in the (original) sample.

CCXR:

435/6

WEST

Generate Collection

L2: Entry 5 of 6

File: USPT

Jul 8, 1993

DOCUMENT IDENTIFIER: US 5225932 A

TITLE: Process for manipulation of non-aqueous surrounded microdroplets

DEPP:

The number of MD groups found by measurement of fluorescence of individual MD groups to contain $n=2$, $n=3$, etc. enzyme labeled specific binding molecules is then used to compute a best value of n for each range (interval) of $V_{subgroup}$ values, and then to compute the best value of ρ by applying the equation ##EQU17## which is the intermediate of the assay, thereby being the number of analyte entities per volume in the diluted sample. It is straightforward to then compute a correction factor, $f_{sub.D}$, ##EQU18## for the dilution during the MD creation process, and thereby, to obtain the concentration, $\rho_{sub.analyte}$, of analyte entity in the (original) sample.

CCXR:

435/6

L2 ANSWER 12 OF 17 BIOSIS COPYRIGHT 2001 BIOSIS DUPLICATE 6
AN 1997:366491 BIOSIS
DN PREV199799858424
TI Visual pigment gene structure and expression in human retinae.
AU Yamaguchi, Tomohiko; Motulsky, Arno G.; Deeb, Samir S. (1)
CS (1) Dep. Med., Univ. Washington, Seattle, WA 98195 USA
SO Human Molecular Genetics, (1997) Vol. 6, No. 7, pp. 981-990.
ISSN: 0964-6906.
DT Article
LA English
AB We determined the genotypes of the X-chromosome-linked red/green color

WEST**End of Result Set**

Generate Collection

L4: Entry 1 of 1

File: USPT

Dec 22, 1998

DOCUMENT-IDENTIFIER: US 5851760 A

TITLE: Method for generation of sequence sampled maps of complex genomes

DEPR:

It was found that the prehybridization of the RNA probes with a high concentration of human repetitive sequences, as hereinabove described, was sufficient to completely block hybridization of most of these frequencies, and was sufficient for eliminating most of these artifactual linkages. However, the analysis of several large contigs mapping to human chromosome 11 generated by this analysis has revealed several cosmid clones which were included in a contig but which could not be substantiated based on the result of restriction mapping and hybridization analysis. This artifact may be the result of cryptic low-frequency repetitive or redundant sequences present in this region of the genome, or could be the result of genomic sequences which are unstable and deleted or rearrange when cloned in *E. coli*. Evidence for the latter sequences, isolated through screening non-amplified cosmid libraries, has been found in the analysis of the human CD3 locus [Evans et al., Immunogen, Supra]. However, it should be noted that the multiplex technique of the present invention, when carried to completion using both T3 and T7 mixed RNA probes, generates data that is internally redundant in that both members of a linked pair should cross-hybridize with one another. Thus, further refinement of this approach should eliminate most serious artifacts arising during multiplex clone analysis.

COOR:435/6**ORPL:**

Lichter, et al., "Rapid Detection Of Human Chromosome 21 Abberations By in situ Hybridization," Proc. Natl. Acad. Sci. (USA), 85:9664-9668 (1988).

correction before data

Trying 31.40.169.2...Open

Welcome to STN International! Enter x:x

LOGINID:asptal165jxl

PASSWORD:

TERMINAL ENTER 1, 2, 3, OR 4 :2

* * * * * Welcome to STN International * * * * *

NEWS 1 Web Page URLs for STN Seminar Schedule - N. America
NEWS 2 Sep 29 The Philippines Inventory of Chemicals and Chemical
Substances (PICCS) has been added to CHEMLIST
NEWS 3 Oct 27 New Extraction Code PAX now available in Derwent
Files
NEWS 4 Oct 27 SET ABBREVIATIONS and SET PLURALS extended in
Derwent World Patents Index files
NEWS 5 Oct 27 Patent Assignee Code Dictionary now available
in Derwent Patent Files
NEWS 6 Oct 27 Elassoc Key Serials Dictionary and Echoing added to
Derwent Subscriber Files WPIDS and WPIX
NEWS 7 Nov 29 Derwent announces further increase in updates for DWPI
NEWS 8 Dec 3 French Multi-Disciplinary Database PASCAL Now on STN
NEWS 9 Dec 3 Trademarks on STN - New DEMAS and EUMAS Files
NEWS 10 Dec 15 2001 STN Pricing
NEWS 11 Dec 17 Merged CEABA-VTS for chemical engineering and
Biotechnology
NEWS 12 Dec 17 Corrosion Abstracts on STN
NEWS 13 Dec 17 SYNTHLINE from Prouis Science now available on STN
NEWS 14 Dec 17 The CA Lexicon available in the CAPLUS and CA files
NEWS 15 Jan 05 AIDSLINE is being removed from STN
NEWS 16 Jan 29 Webcast on CA LEXICON

NEWS EXPRESS FREE UPGRADE 5.0e FOR STN EXPRESS 5.0 WITH DISCOVER!
(WINDOWS) NOW AVAILABLE
NEWS HOURS STN Operating Hours Plus Help Desk Availability
NEWS INTER General Internet Information
NEWS LOGIN Welcome Banner and News Items
NEWS PHONE Direct Dial and Telecommunication Network Access to STN
NEWS WWW CAS World Wide Web Site (general information)

Enter NEWS followed by the item number or name to see news on that
specific topic.

All use of STN is subject to the provisions of the STN Customer
agreement. Please note that this agreement limits use to scientific
research. Use for software development or design or implementation
of commercial gateways or other similar uses is prohibited and may
result in loss of user privileges and other penalties.

* * * * * STN Columbus * * * * *

FILE 'HOME' ENTERED AT 16:18:54 ON 01 FEB 2001

=> file biosis caplus medline scisearch

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	0.15	0.15

FILE 'BIOSIS' ENTERED AT 16:19:14 ON 01 FEB 2001
COPYRIGHT (C) 2001 BIOSIS (R)

FILE 'CAPLUS' ENTERED AT 16:19:14 ON 01 FEB 2001
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP UNAGTERMS" FOR DETAILS.
COPYRIGHT (C) 2001 AMERICAN CHEMICAL SOCIETY (ACS)

FILE 'MELLINE' ENTERED AT 18:19:14 ON 01 FEB 2001

FILE 'SCISEARCH' ENTERED AT 18:19:14 ON 01 FEB 2001

COPYRIGHT (C) 2001 Institute for Scientific Information (ISI) (P)

=> s (filter or artifact or anomaly) and (gene (array or chip))

MISSING OPERATOR 'GENE (ARRAY'

The search profile that was entered contains terms or nested terms that are not separated by a logical operator.

=> s (filter or artifact or anomaly) and (gene w (array or chip))

MISSING OPERATOR 'W (ARRAY'

The search profile that was entered contains terms or nested terms that are not separated by a logical operator.

=> s (filter or artifact or anomaly) and (gene adj (array or chip))

MISSING OPERATOR 'ADJ (ARRAY'

The search profile that was entered contains terms or nested terms that are not separated by a logical operator.

=> s (filter or artifact or anomaly) and ((gene array) or (gene chip))

3 FILES SEARCHED...

L1 39 (FILTER OR ARTIFACT OR ANOMAL?) AND ((GENE ARRAY) OR (GENE CHIP))

=> dup rem l1

PROCESSING COMPLETED FOR L1

L2 17 DUP REM L1 (21 DUPLICATES REMOVED)

=> d l1 sub ak 1-17

L2 ANSWER 1 OF 17 CABLUS COPYRIGHT 2001 ACS

AN 2001:44425 CABLUS

TI Number and Variations of the Red and Green Visual Pigment Genes in Japanese Men with Normal Color Vision

AU Hayashi, S.; Ueyama, H.; Tanaka, S.; Yamada, S.; Kani, K.

CS Otsu, Japan

SO Jpn. J. Ophthalmol. (2001), 45(1), 60-67

CODEN: JOPHA7; ISSN: 0021-5155

PB Elsevier Science Inc.

DT Journal

LA English

AB Purpose: We analyzed the red/green visual pigment genes in color-normal Japanese men to understand the relationship between color **anomalies** and genetic defects. Methods: DNA from 120 color-normal Japanese men was subjected to polymerase chain reaction (PCR)-amplification for exons 2-5 of the red/green visual pigment genes and the PCR products were sequenced. The red:green gene ratios were estd. from the sequencing electropherograms of exon 5 and also from MvaI-restriction fragment anal. of the same exon. The first gene and the downstream genes in the pigment **gene array** were sep. analyzed by PCR, direct sequencing, and/or single-strand conformation polymorphisms. Results: The red:green gene ratios estd. from the ratios of peak heights of nucleotides on the sequencing electropherograms coincided with those estd. from the MvaI-restriction fragment anal. Among the subjects analyzed, they were 1:1 in 43 (n = 52), 1:2 in 41 (n = 49), 1:3 in 6 (n = 7), and 1:>3 in 9 (n = 11). The first gene in the pigment **gene arrays** was red in all subjects. Only 1 subject (N12) had a green-red hybrid gene. Exons 2 and 4 had 2 haplotypes each, but exon 3 was highly polymorphic. Exon 5 of the green genes had one polymorphism at codon 293 with a frequency of 32. Conclusions: The features of visual pigment genes in color-normal Japanese men were

revealed. The data on establishing techniques may be useful for analyzing these genes in color-deficient subjects in the Japanese population.

LE ANSWER 2 OF 17 CAPLUS COPYRIGHT 2001 ACS
 AN 2001091115L6 CAPLUS
 IN 134:52249
 TI System for eliminating background in **gene chip** array
 analysis
 IN Bliton, Allison C.
 PA Genomic Solutions Inc., USA
 SC Pat. Int. Appl., 9 pp.
 CODEN: P1XXD2
 DT Patent
 LA English
 FAN.ENT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000/010250	A1	20000128	WO 2000-US15695	20000616

W:	AE, AL, AM, AT, AU, AZ, BA, BB, BG, BP, BY, CA, CH, CN, CR, CU,
	CG, DE, DK, DM, EE, EG, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL,
	IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA,
	MD, MG, MK, MN, MW, ME, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI,
	SK, SL, TN, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM,
	AD, BY, CG, CE, CO, DD, DU, EE, TT, TH
RW:	GH, GM, GN, HS, HW, HU, ID, IL, IS, IT, LU, MC, NL, PT, SE, BF, BJ,
	DE, DK, ES, FI, FR, GE, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ,
	AF, AG, AI, AM, AN, AO, AP, AR, AS, AT, AU, AW, AX, AY, AZ, BA,

PRAI	US	1999-140063	19990613
	US	2000-595332	20000616

AB A system to eliminate background in optically scanned samples is disclosed which selectively blocks excitation or emission light through the use of **filters.**

RE.CNT 3
RE

(1) Hoyt; US 5043129 A 1990 CAPLUS
(2) Sarpas; US 5930943 A 1999
(3) Trost; US 6066245 A 2000 CAPLUS

L2 ANSWER 3 OF 17 CAPJUS COPYRIGHT 2001 ACS DUPLICATE 1
AN 2:00:856693 CAPJUS

TI A pulmonary rat **gene array** for screening altered
expression profiles in air pollutant-induced lung injury
AU Nagaraj, Srikanth S.; Schladweiler, Hette C. J.; Kodavanti, Urmila P.
CS Curriculum in Toxicology, University of North Carolina, Chapel Hill, NC,
USA
SC Inhalation Toxicol. (2000), 18(12), 1239-1254
CODEN: INHTE5; ISSN: 0895-8378
PB Taylor & Francis
DT Journal
LA English
AB Pulmonary tissue injury and repair processes involve complex and
coordinated cellular events such as necrosis, inflammation, cell
growth/differentiation, apoptosis, and remodeling of extracellular matrix.
These processes are regulated by expression of multiple mediator genes.
Comm. available microarray blots and slides allow screening of hundreds to
thousands of genes in a given tissue or cell prepn. However, often these
blots do not contain cDNAs of one's interest and are difficult to
interpret. In order to analyze the tissue expression profile of a large
no. of genes involved in pulmonary injury and pathol., we developed a rat
gene array filter using array technol. This
array consisted of 27 genes representing inflammatory and
anti-inflammatory cytokines, growth factors, adhesion molts., stress
proteins, transcription factors and antioxidant enzymes; 3 neg. controls,
and 2 blank spots. Using rat gene-specific polymerase chain reaction
(PCR) primer pairs, cDNAs for these genes were amplified and cloned into a
TA vector. Plasmids with recombinant cDNA inserts were purified and
blotted onto a nylon membrane. Lung total RNA was isolated at 3 or 14 h
following intratracheal (IT) exposure of male Sprague Dawley rats to

either saline (control), residual oil fly ash (ROFA; 3.0 mg/kg) or metals found in one installment of ROFA: nickel (NiSO₄; 1.3 μmol/kg) or vanadium (VSO₄; 1.2 μmol/kg). 32P-Labeled cDNA was generated from RNA same.

PE: WT 23

RE

- (1) Barnes, P; Eur Respir J 1998, V12, P221 CAPLUS
- (2) Bittner, M; Nat Genet 1999, V12, P213 CAPLUS
- (4) DePisi, J; Nat Genet 1996, V14, P457 CAPLUS
- (6) Dreher, K; J Toxicol Environ Health 1997, V50, P285 CAPLUS
- (8) Hatch, G; Environ Res 1985, V36, P87 CAPLUS

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 4 OF 17 SCISEARCH COPYRIGHT 2001 ISI (R)

AN 2001:171548 SCISEARCH

GA The Genuine Article (R, Number: 374EF

TI Fundamentals of DNA hybridization arrays for gene expression analysis

AU Freeman W M; Robertson L C; Vrana P E (Reprint)

CS WAKE FOREST UNIV, SCH MED, DEPT PHYSIOL & PHARMACOL, MED CTR BLVD, WINSTON SALEM, NC 27157 (Reprint); WAKE FOREST UNIV, SCH MED, DEPT PHYSIOL & PHARMACOL, WINSTON SALEM, NC 27157

CYA USA

SO BIOTECHNIQUES, (NOV 2000) Vol. 19, No. 5, pp. 1042-9.

Publisher: EATON PUBLISHING CO, 154 E. CENTRAL ST, NATICK, MA 01760.

ISSN: 0736-6205.

DT General Review: Journal

FS LIFE

LA English

REC Reference Count: 17

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB DNA hybridization arrays [also known as macroarrays, microarrays and/or high-density oligonucleotide arrays (**Gene Chips**(TM))]. Bring gene expression analysis to a genomic scale by permitting investigators to simultaneously examine changes in the expression of laterally thousands of genes. For hybridization arrays, the general approach is to immobilize gene-specific sequences (probes) on a solid state matrix (nylon membranes, glass microscope slides, silicon/ceramic chips). These sequences are then probed with labeled copies of nucleic acids from biological samples (targets). The underlying theory is that the greater the expression of a gene, the greater the amount of labeled target, and hence, the greater output signal. In spite of the simplicity of the experimental design, there are at least four different platforms and several different approaches to processing and labeling the biological samples. Moreover, investigators must also determine whether they will utilize commercially available arrays or generate their own. This review will cover the status of the hybridization array field with an eye toward underlying principles and available technologies. Further developments and technological trends will also be evaluated.

L2 ANSWER 5 OF 17 CAPLUS COPYRIGHT 2001 ACS

DUPLICATE 2

AN 2001:133592L CAPLUS

TI Correlation of Gene Structure and Psychophysical Measurement in Red-Green Color Vision Deficiency in Chinese

AU Zhang, Q.; Xiao, X.; Shen, H.; Li, S.; Jiang, F.

CS National Ophthalmological Labs and Zhongshan Ophthalmic Center, Ocular Genetics and Molecular Biology, Sun Yat-sen University of Medical Sciences, Canton, Peop. Rep. China

SO Jpn. J. Ophthalmol. (2000), 44(6), 598-600

CBRN: JOPPA7; ISSN: 0021-5155

PB Elsevier Science Inc.

DT Journal

LA English

AB Purpose: To study the correlation of genotype for X-linked red-green

gene array with color vision phenotype in 58 subjects

with red-green color vision deficiency. Methods: The mol. structure of red and green pigment genes on 58 X chromosomes was studied exon-by-exon by using heteroduplex-SSCP anal. and sequencing. The color vision of these subjects was detd. by a Neitz **anomaloscope**. Results: Variations in the red and green pigment genes were detected in 43 subjects and a

hybrid gene was found in 27 subjects. About 50% of the fusion sites occurred at intron 2-3. All 3 **anomalous** trichromats with intron 4 fusion were mild type but another 3 with intron 2-3 fusion were severe type. No subjects with mild type of color vision defects had a fusion site at intron 2-3 or its upstream. Three subjects with complete deletion of the green pigment gene manifested deuteranomaly. Conclusions: Protans can be differentiated from deuters on the basis of genotype. It is still difficult to establish a clear correlation of different **anomalous** trichromats with genotype. The fusion site of a hybrid gene affects the phenotype to some degree. Intron 2-3 is the common place for gene crossover.

PE.CNT 12

RE

- (1) Asenjo, A; Neuron 1994, V12, P131 CAPLUS
 - (2) Deel, S; Am J Hum Genet 1992, V51, P687 CAPLUS
 - (3) Hayashi, T; Nat Genet 1998, V22, P91 CAPLUS
 - (4) Nathans, J; Science 1984, V232, P193 CAPLUS
 - (5) Nathans, J; Science 1984, V232, P203 CAPLUS
- ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 6 OF 17 BIOSIS COPYRIGHT 2001 BIOSIS DUPLICATE 3

AN 1999:1304047 BIOSIS

DN PREV199901304047

TI Direct visual resolution of gene copy number in the human photopigment **gene array**.

AU Wolf, Stephan; Sharpe, Lindsay T. (1); Schmidt, Hans-Juergen A.; Knau, Holger; Weitz, Sandra; Kirschis, Petra; Prustka, Annemarie; Erenner, Eberhart; Lichter, Peter; Wissinger, Bernd

CS (1) Forschungsstelle fuer Experimentelle Ophthalmologie, Universitaets-Augenklinik, Roentgenweg 11, D-72076, Tuebingen, Germany

SC IOVS, (June, 1999) Vol. 40, No. 7, pp. 1585-1589.

ET Article

LA English

SL English

AB PURPOSE. To visualize by direct fluorescent in situ hybridization the entire human visual pigment **gene array** in single X-chromosome fibers and to compare the results with values obtained by other molecular techniques. METHODS. The size of the opsin **gene array** on the X-chromosome in eight male subjects was investigated by (i) direct visual in situ hybridization (DIRVISH) on elongated DNA fibers; (ii) quantitation of genomic restriction fragments after Southern blot hybridization; (iii) quantitation of restriction fragment length polymorphism after PCR amplification (PCR/RFLP); and (iv) sizing of NotI fragments by pulsed field gel electrophoresis and Southern blot detection. Each male subject's color vision was assessed by Rayleigh matches on a Nagel Type 1 **anomaloscope**. RESULTS. The number of genes resolved by the DIRVISH protocol, which ranges from 1 to 6, agrees exactly with the **gene array** sizes obtained in the same male subjects from pulsed field gel electrophoresis, but differs from the estimates derived from the commonly used indirect Southern blot hybridization and PCR/RFLP quantitation methods. In particular, the PCR/RFLP method overestimates the copy number in all but the smallest arrays. CONCLUSIONS. Visualization of the X-chromosome opsin **gene array** by DIRVISH provides a new, direct method for obtaining exact copy numbers and helps to resolve the controversy about the range and the average visual pigment gene number in the human population in favor of smaller average array sizes.

L2 ANSWER 7 OF 17 BIOSIS COPYRIGHT 2001 BIOSIS

AN 2000:143951 BIOSIS

DN PREV20000143951

TI Analysis of gene expression following traumatic brain injury using gene expression array technology.

AU Harrison, S. M. W. (1); Davis, B. M. (1); Sullivan, P. G. (1); Scheff, S. W. (1)

CS (1) Dept. of Anatomy and Neurobiology, University of Kentucky College of Medicine, Lexington, KY, 40536 USA

SC Society for Neuroscience Abstracts., (1999) Vol. 25, No. 1-2, pp. 821. Meeting Info.: 29th Annual Meeting of the Society for Neuroscience. Miami Beach, Florida, USA October 23-28, 1999 Society for Neuroscience

1. ISSN: 0191-5295.
 DT Conference
 LA English
 SL English

LE ANSWER 3 OF 17 SCISEARCH COPYRIGHT 2001 ISI (R)
 AN 1999:412517 SCISEARCH
 GA The Genuine Article (R) Number: 258MM
 TI Application of DNA arrays to toxicology
 AU Rockett J C (Reprint); Dix D J
 CS US EPA, NATL HLTH & ENVIRONM EFFECTS RES LAB, REPRODUCT TOXICOL DIV MI72, RES TRIANGLE PK, NC 27711 (Reprint)
 CYA USA
 SO ENVIRONMENTAL HEALTH PERSPECTIVES, (AUG 1999) Vol. 107, No. 8, pp. 641-645.
 PUBLISHER: US DEPT HEALTH HUMAN SCIENCES PUBLIC HEALTH SCIENCE, NATL INST HEALTH, NATL INST ENVIRONMENTAL HEALTH SCIENCES, PO BOX 12233, RES TRIANGLE PK, NC 27709-2233.
 ISSN: 0091-6765.

DT Article: Journal
 FS LIFE: AGRI
 LA English
 REC Reference Count: 14
 ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB DNA array technology makes it possible to rapidly genotype individuals or quantify the expression of thousands of genes on a single **filter** or glass slide, and holds enormous potential in toxicologic applications. This potential led to a U.S. Environmental Protection Agency-sponsored workshop titled "Application of Microarrays to Toxicology" on 7-8 January 1999 in Research Triangle Park, North Carolina. In addition to providing state-of-the-art information on the application of DNA or gene microarrays, the workshop catalyzed the formation of several collaborations, committees, and user's groups throughout the Research Triangle Park area and beyond. Potential application of microarrays to toxicologic research and risk assessment include genome-wide expression analyses to identify gene-expression networks and toxicant-specific signatures that can be used to define mode of action, for exposure assessment, and for environmental monitoring. Arrays may also prove useful for monitoring genetic variability and its relationship to toxicant susceptibility in human populations.

LE ANSWER 3 OF 17 CAPLUS COPYRIGHT 2001 ACS
 AN 1999:672643 CAPLUS
 DN 119:272643
 TI Biomolecular processor for isolation and purifn. of nucleic acids
 IN Fields, Robert E.
 PA USA
 SO PET Int. Appl., 36 pp.
 CODEN: PIXXD2

DT Patent
 LA English
 FAN EN: 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9842874	A2	19981001	WO 1998-US6029	19980323
	WO 9842874	A3	19981023		
	WO	AL, AI, AP, AU, AC, EA, BB, BG, BP, BY, CA, CH, CN, CU, CZ, DE, DK, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RB, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
	PW:	GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG			
AU	9867790	A1	19981020	AU 1998-67790	19980323
EP	972090	A2	20000119	EP 1998-913175	19980323
	P:	AT, BE, CH, IE, IK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI			
EPAI	US 1997-41237		19970324		

AB A process and app. are described for isolating and purifying nucleic acids and other target mols. directly from blood, plasma, urine, cell cultures and the like by totally automated means, without centrifugation, aspiration or vacuum. After mixing and heating a nucleic acid contg. sample with lysis reagent in an environmentally isolated compartment, nucleic acids are absorbed onto a binding **filter** and eluted in a small vol. using heated elution reagent. A preferred embodiment purifies nucleic acids and automatically detects target sequences from a sample of fresh blood. Another embodiment purifies target mols. from a multitude of samples held in microtiter plates. Test kits for each embodiment include disposable isolation and detection devices and assocd. reagents.

L2 ANSWER 10 OF 17 BIOSIS COPYRIGHT 2001 BIOSIS DUPLICATE 4
 AN 1999:39417 BIOSIS
 DN PREV19990039417
 TI Red, green, and red-green hybrid pigments in the human retina: Correlations between deduced protein sequences and psychophysically measured spectral sensitivities.
 AU Sharpe, Lindsay T. (1); Stockman, Andrew; Mägle, Herbert; Mägle, Holger; Klausen, Gert; Reither, Andreas; Nathans, Jeremy
 CS (1) Forschungsstelle Exp. Ophthalmol., Univ.-Augenklin. Abteilung II, D-72076 Tuebingen Germany
 SO Journal of Neuroscience, Dec. 1, 1999 Vol. 19, No. 23, pp. 10059-10069. ISSN: 0270-6474.
 DT Article
 LA English
 AB To analyze the human red, green, and red-green hybrid cone pigments in vivo, we studied 41 male dichromats, each of whose X-chromosome carries only a single visual pigment gene (single-gene dichromats). This simplified arrangement avoids the difficulties of complex opsin **gene arrays** and overlapping cone spectral sensitivities present in trichromats and of multiple genes encoding identical or nearly identical cone pigments in many dichromats. It thus allows for a straightforward correlation between each observer's spectral sensitivity measured at the fovea and the amino acid sequence of his visual pigment. For each of the 41 single-gene dichromats we determined the amino acid sequences of the X-linked cone pigment as deduced from its gene sequence. To correlate these sequences with spectral sensitivities in vivo, we determined the Rayleigh matches to different red/green ratios for 23 single-gene dichromats and measured psychophysically the spectral sensitivity of the remaining green (middle wavelength) or red long wavelength) cones in 17 single-gene dichromats. Cone spectral sensitivity maxima obtained from subjects with identical visual pigment amino acid sequences show up to a approx3% variation from subject to subject, presumably because of a combination of inexact or not corrections for variation in preretinal absorption, variation in photopigment optical density, optical effects within the photoreceptor, and measurement error. This variation implies that spectral sensitivities must be averaged over multiple subjects with the same genotype to obtain representative values for a given pigment. The principal results of this study are that (1) approx54% of the single-gene protanopes (and approx19% of all protanopes) possess any one of several 5'red-3'green hybrid genes that encode **anomalous** pigments and that would be predicted to produce protanomaly if present in **anomalous** trichromats; (2) the alanine-serine polymorphism at position 180 in the red pigment gene produces a spectral shift of approx2.7 nm; (3) for each exon the set of amino acids normally associated with the red pigment produces spectral shifts to longer wavelengths, and the set of amino acids normally associated with the green pigment produces spectral shifts to shorter wavelengths; and (4) changes in exons 2, 3, 4, and 5 from green to red are associated with average spectral shifts to long wavelengths of approx1 nm (range, -3.5 to 2.5 nm), approx2.3 nm (range, -0.5 to 7 nm), approx2.8 nm (range, -0.5 to 6 nm), and approx24.9 nm (range, 22.2-27.6 nm).

L2 ANSWER 11 OF 17 BIOSIS COPYRIGHT 2001 BIOSIS DUPLICATE 5
 AN 1999:148500 BIOSIS
 DN PREV199900148500
 TI Individual variations in color vision and its molecular biology.

AU Kitahara, Kenji (1)
 CS (1) Dep. Ophthalmology, Tokei Univ. Sch. Med., 3-25-8 Niishi-shinbashi,
 Minato-ku, Tokyo 106-8461 Japan
 SO Nippon Ganka Gakkaï Zasshi, (Dec., 1999) Vol. 102, No. 12, pp. 837-849.
 ISSN: 0027-0203.
 IT Article
 LA Japanese
 SL Japanese; English.
 AB Individual variations in normal color vision and congenital red-green
 color vision defects in Japanese males were investigated using both
 psychophysics and molecular biology techniques. 1. Normal color vision. We
 studied 41 Japanese males who were diagnosed as having normal color vision
 using the Ishihara plates test and Nagel model I **anomaloscope**.
 The structure of the **gene arrays** of the X-linked L-
 and M-pigment genes was determined using quantitative PCR-SSCP (polymerase
 chain reaction-single strand conformation polymorphism). We found the
 following variations of the number of M-pigment genes: 27 (66%) of these
 men had only one M-pigment gene, 10 (40%) had two, 13 (18%) had three and
 1 (4%) had four. Two common polymorphisms were found at amino acid residue
 180 of both L- and M-opsin, of the total 58 (78%) were Ser and the other
 16 (12%) were Ala in the L-pigment and of the total 65 (91%) were Ala and
 the other 7 (13%) were Ser in the M-pigment. The Rayleigh match midpoints
 fell within the normal range, however there were two fairly distinct
 groups with consistent differences in each group. The mean values of the
 proportion of red in a mixture of red and green were 0.564 ± 0.026 (mean
 \pm standard deviation). Correlation was found only between the Rayleigh
 match midpoint and the polymorphism at residue 180 of L-pigment. In order
 to estimate the variations of L/M cone ratio in the retinae the spectral
 sensitivities using heterochromatic flicker method were measured. Using
 the hypothesis that the luminosity function is proportional to the sum of
 L- and M-cone spectral sensitivity ($k L(\lambda) + M(\lambda)$), the
 constant k values were obtained. The k values for the subjects with Ser180
 and Ala180 L-pigment were 1.89 ± 1.44 and 1.33 ± 1.02 respectively.
 Furthermore, in order to study the variation of information processing
 system, the spectral sensitivities for 1 degree, 200-ms test flash on a
 white background were measured. Using the hypothesis that the spectral
 sensitivity is proportional to the difference of L- and M-cone spectral
 sensitivity ($L(\lambda) - k' M(\lambda)$), the k' values were obtained. The
 k' values for the subjects with Ser180 and Ala180 L-pigment were
 1.38 ± 0.36 and 1.42 ± 0.97 respectively. As a result, it was suggested that
 there are individual variations in both the L/M cone ratio and the color
 opponent system. 2. Congenital red-green color vision deficiencies. We
 studied the structure of the **gene arrays** of the
 X-linked L- and M-pigment genes and investigated the relationship between
 genotype and phenotype in 21 Japanese males comprising 4 protanopia, 6
 protanomaly, 7 deutanopia and 4 deutanomaly. All of the protan
 subjects had 5' L-M fusion gene with/without the M gene. All of the
 deutan subjects had a normal L gene with/without 5' M-L fusion gene.
 Genotype agreed with phenotype in 3 of 10 protan subjects and 10 of 11
 deutan subjects. Two of them were diagnosed as abnormal trichromatism in
 spite of having only one gene. One of them was diagnosed as dichromatism
 in spite of having two genes that encoded spectrally different pigments.
 As a result, it was felt that the diagnosis of dichromasy and abnormal
 trichromasy with an **anomaloscope** has limitations.

L2 ANSWER 12 OF 17 BIOSIS COPYRIGHT 2001 BIOSIS DUPLICATE 6
 AN 1997:366491 BIOSIS
 DN PREV199799658424
 TI Visual pigment gene structure and expression in human retinae.
 AU Yamaguchi, Tomohiko; Motulsky, Arno S.; Deeb, Samir S. (1)
 CS (1) Dep. Med., Univ. Washington, Seattle, WA 98195 USA
 SO Human Molecular Genetics, (1997) Vol. 6, No. 7, pp. 981-990.
 ISSN: 0964-6906.
 IT Article
 LA English
 AB We determined the genotypes of the X-chromosome-linked red/green color
 vision genes by a novel PCR/SSCP-based method and assessed expression by
 mRNA analysis in retinae of 51 unselected post mortem eye specimens from
 Caucasian males of unknown color vision status. All individuals had a

single red long-wave pigment gene and one or more (and a large of two green middle-wave pigment genes. Four males had 5 'green-red' hybrid genes in addition to normal red and green pigment genes. These findings are consistent with earlier studies on human visual pigment gene structure using Southern blotting and with a recent study using pulsed-field electrophoresis. We interpret claims of much larger numbers of red, green and green-red hybrid genes to be technical **artifacts**. The ratio of expressed red to green pigment retinal mRNA varied widely 1-10 with a mode of 4:1 and was not correlated with that of red to green pigment genes. In one individual with a green-red hybrid gene in addition to normal red and green pigment genes, the normal red pigment gene and the hybrid gene were both expressed, but the normal green gene was not. This person presumably had deuteranomalous color genes. These two individuals presumably had normal color vision. We interpret the failure to express their vision. Two with green-red hybrid genes expressed the normal red and green pigment genes, but not the hybrid genes. These two individuals presumably had normal color vision. We interpret the failure the express their green-red hybrid genes to be caused by their location at a more distal position in the visual pigment **gene array**.

LE ANSWER 13 OF 17 CAPLUS COPYRIGHT 2001 ACS
 AN 1337:131010 CAPLUS
 TI Thermodynamics of duplex formation and mismatch discrimination on photolithographically synthesized oligonucleotide arrays.
 AU Fornace, Jonathan B.; Walton, Ian D.; Stern, David; Rava, Richard P.; Trulsson, Marc O.
 CS Affymetrix, Santa Clara, CA, 95051, USA
 SO Book of Abstracts, 213th ACS National Meeting, San Francisco, April 13-17 1997, COMP-312 Publisher: American Chemical Society, Washington, D. C. CODEN: AAGAAA
 DT Conference; Meeting Abstract
 LA English
 AB Oligonucleotide probes immobilized on solid supports are finding increasingly widespread application in genetic anal. To address the fundamental kinetic and thermodyn. aspects of these systems, we have investigated duplex formation between a 20 base oligonucleotide and 240 probe sequences ranging from 10 to 20 bases in length on an Affymetrix **Gene Chip** array. Multiple kinetic components are obsd. in the duplex assocn. and dissocn. kinetics of each probe sequence. The dominant kinetic component in the assocn. data is similar to predicted soln. kinetics, but slower components are obsd. as well. A distribution of dissocn. rate consts. differing by as much as two orders of magnitude is obsd. for a given probe sequence. Equil. melt curves likewise show multicomponent behavior, and melting temps. are consistently lower than those of corresponding soln. phase species. The effects of probe length heterogeneity, probe surface d., and mass transport **artifacts** on the obsd. data will be discussed.

LE ANSWER 14 OF 17 BIOSIS COPYRIGHT 2001 BIOSIS DUPLICATE 7
 AN 1995:462177 BIOSIS
 DN PREV19959476477
 TI Polymorphism in the number of genes encoding long-wavelength-sensitive cone pigments among males with normal color vision.
 AU Neitz, Maureen; Neitz, Jay (1); Grishok, Alla
 CS (1) Dep. Ophthalmol., Med. Coll. Wis., 8701 Watertown Plank Road, Milwaukee, WI 53226-0503 USA
 SO Vision Research, 1995 Vol. 35, No. 17, pp. 2399-2407. ISSN: 0042-6989.
 DT Article
 LA English
 AB Examination by direct DNA sequence analysis of the X-linked visual pigment genes in 27 males with normal color vision reveals that almost half have two or more different genes encoding a long-wavelength-sensitive cone pigment. This is counter to the conventional theory proposed from results of Southern hybridization studies that there is a single long-wave pigment gene per X-chromosome. Further, the sequences and consideration of the structure of the X-linked pigment **gene array** suggest that the majority of the observers (as many as 2/3) have hybrid (or fusion) genes like those that have been proposed to underlie color

anomaly. In some observations the long-wave hybrid genes contain a substantial amount of middle-wave sequence, e.g. five carriers have hybrid long-wave genes that contain middle-wave sequences that include exon 4. Three of these five have the hybrid as their only long-wave gene, and thus have no other gene that could potentially encode a long-wave pigment. In these subjects, it is the hybrid gene that produces their normal long-wavelength-sensitive cone pigment. The high frequency of hybrid genes indicates that they are normal variant forms of the long-wave gene. Contrary to what is commonly believed, the introduction and the expression of hybrid genes is not sufficient to cause color vision defects.

L2 ANSWER 15 OF 17 BIOSIS COPYRIGHT 2001 BIOSIS DUPLICATE 9
 AN 1999:4383 BIOSIS
 DN PREV19993514383
 TI Genotype-phenotype relationships in human red/green color-vision defects: Molecular and psychophysical studies.
 AU Deeb, Samir S. (1); Lindsey, Delwin T.; Ribiya, Yuzo; Sanocki, Elizabeth; Winderickx, Chris; Teller, David A.; Motulsky, Arno G.
 CS (1) Dep. Genetics, SK-50, Univ. Wash., Seattle, Wash. 98195
 SO American Journal of Human Genetics, (1999) Vol. 51, No. 4, pp. 687-700.
 ISSN: 0002-3297.
 DT Article
 LA English
 AB The relationship between the molecular structure of the X-linked red and green visual pigment genes and color-vision phenotype as ascertained by **anomaloscopy** was studied in 64 color-defective males. The great majority of red-green defects were associated with either the deletion of the green-pigment gene or the formation of 5' red-green hybrid genes or 5' green-red hybrid genes. A rapid PCR-based method allowed detection of hybrid genes, including those undetectable by Southern blot analysis, as well as more precise localization of the fusion points in hybrid genes. Protan color-vision defects appeared always associated with 5' red-green hybrid genes. Carriers of single red-green hybrid genes with fusion in introns 1-4 were protanopes. However, carriers of hybrid genes with red-green fusions in introns 2, 3, or 4 in the presence of additional normal green genes manifested as either protanopes or protanomalous trichromats, with the majority being protanomalous. Deutan defects were associated with green-pigment gene deletions, with 5' green-red hybrid genes, or, rarely, with 5' green-red hybrid genes. Complete green-pigment gene deletions or green-red fusions in intron 1 were usually associated with deuteranopia, although we unexpectedly found three carriers of a single red-pigment gene without any green-pigment genes to be deuteranomalous trichromats. All but one of the other deuteranomalous subjects had green-red hybrid genes with intron 1, 2, 3, or 4 fusions, as well as several normal green-pigment genes. The one exception has a possibly normal **gene array**, presumably with a more subtle mutation. Amino acid differences in exon 5 largely determine whether a hybrid gene will be more redlike or more greenlike in phenotype. Various discrepancies as to severity (dichromacy or trichromacy) remain unexplained but may arise because of variability of expression, postreceptoral variation, or both. When phenotypic color-vision defects exist, the kind of defect (protan or deutan) can be predicted by molecular analysis. Red-green hybrid genes are probably always associated with protan color-vision defects, while the presence of green-red hybrid genes may not always manifest phenotypically with color-vision defects. Four subjects who were found to have 5' green-red hybrid genes in addition to normal red- and green-pigment genes had normal color vision as determined by **anomaloscopy**. These were discovered among a group of 129 Caucasian males who had been recruited as volunteers for a vision study. We hypothesize that green-red hybrid genes in a more distal (3') position of a **gene array** that includes one or more normal green genes may not be expressed sufficiently to measurably affect color vision.

L2 ANSWER 16 OF 17 BIOSIS COPYRIGHT 2001 BIOSIS DUPLICATE 9
 AN 1999:431539 BIOSIS
 DN PREV1999351431539
 TI MOLECULAR PATTERNS OF X CHROMOSOME-LINKED COLOR VISION GENES AMONG 134 MEN OF EUROPEAN ANCESTRY.

AU DRUMMOND-BORG M; DEER S; MCTULSKY A G
 CS CENT. INHERITED DISEASES, UNIV. WASHINGTON, SEATTLE, WASH. 98195.
 SO PROC NATL ACAD SCI U S A, (1989) 86 (13), 3883-3887.
 CODEN: PNASAG. ISSN: 0027-8424.
 ES EN: OLD
 LA English
 AB We used Southern blot hybridization to study X chromosome-linked color vision genes encoding the apoproteins of red and green visual pigments in 104 unselected Caucasian men. One hundred and thirteen individuals (84.3%) had a normal arrangement of their color vision pigment genes. All had one red pigment gene; the number of green pigment genes ranged from one to five with a mode of two. The frequency of molecular genotypes indicative of normal color vision (84.3%) was significantly lower than had been observed in previous studies of color vision phenotypes. Color vision defects can be due to deletions of red or green pigment genes or due to formation of hybrid genes comprising portions of both red and green pigment genes [Nathans, J., Piantanida, T. R., Eday, R. L., Shows, T. B., Day, & Hogness, D. M. (1986) Science 232, 203-210]. Characteristic **anomalous** patterns were seen in 15 (14.2%) individuals: 7 (5.2%) as patterns characteristic of deuteranomaly (mild defect in green color perception), 2 (1.5%) had patterns characteristic of deuteranopia (severe defect in green color perception), and 6 (4.5%) had protan patterns (the red perception defects protanomaly and protanopia cannot be differentiated by current molecular methods). Previously undescribed hybrid gene patterns consisting of both green and red pigment gene fragments in addition to normal red and green genes were observed in another 6 individuals (4.5%). Only 2 of these patterns were considered as deuteranomalous. Thus, DNA testing detected **anomalous** color vision pigment genes at a higher frequency than expected from phenotypic color vision tests. Some color vision **gene arrays** associated with hybrid genes are likely to mediate normal color vision.

L2 ANSWER 12 OF 17 BIDSIS COPYRIGHT © 91 BIDSIS DUPLICATE 10
 AN 1-89-16731 BIDSIS
 DN EA87:16731

TI MOLECULAR BASIS OF ABNORMAL RED-GREEN COLOR VISION A FAMILY WITH THREE TYPES OF COLOR VISION DEFECTS.

AU DRUMMOND-BORG M; DEER S; MCTULSKY A G
 CS DIV. MED. GENETICS, PG-15, UNIV. WASH., SEATTLE, WASH. 98195.
 SO AM J HUM GENET, (1989) 44 (5), 875-883.
 CODEN: AJHGAG. ISSN: 0002-9297.
 ES EN: OLD
 LA English

AB The molecular nature of three different types of X-linked color-vision defects, protanomaly, deuteranomaly, and protanopia, in a large 3-generation family was determined. In the protanomalous and protanopic males the normal red pigment gene was replaced by a 5' red-3' green fusion gene. The protanomalous male had more red pigment DNA in his fusion gene than did the more severely affected protanopic individual. The deuteranomalous individual had four green pigment genes and 5' green-3' red fusion gene. These results extend those of Nathans et al., who proposed that most red-green color-vision defects arise as a result of unequal cross-over between the red and green pigment genes. The various data suggest that differences in severity of color-vision defects associated with fusion genes are caused by differences in crossover sites between the red and green pigment genes. Currently used molecular methodology is not sufficiently sensitive to define these fusion points accurately, and the specific color-vision defect within the deutan or protan class cannot be predicted. The DNA patterns for color-vision genes of female heterozygotes have not previously been described. Patterns of heterozygotes may not be distinguishable from those of normals. However, a definite assignment of the various color pigment **gene arrays** could be carried out by family study. Two compound heterozygotes for color-vision defects who tested as normal by **anomaloscopy** were found to carry abnormal fusion genes. In addition, a normal red pigment gene was present on one chromosome and at least one normal green pigment gene was present on the other. Thus, the presence of normal green and red pigment genes insured normal color vision. The presence of fusion genes did not grossly influence color

perception in these individuals. A third compound heterozygote had decreased luminosity for yellow in one eye only.

=> s (correction factor)

L3 12926 (CORRECTION FACTOR)

=> s L3 and (dna) and (gene or array or chip or assay)

L4 1 L3 AND (DNA) AND (GENE OR ARRAY OR CHIP OR ASSAY)

=> dup rem L4

PROCESSING COMPLETED FOR L4

L5 15 DUP REM L4 (24 DUPLICATES REMOVED)

=> d his

(FILE 'HOME' ENTERED AT 16:18:54 ON 01 FEB 2001)

FILE 'BIOSIS, CABLUS, MEDLINE, SCISEARCH' ENTERED AT 16:19:14 ON 01 FEB 2001

L1 18 S (FILTER OR ARTIFACT OR ANOMAL?) AND ((GENE ARRAY) OR (GENE CH

L2 17 DUP REM L1 (21 DUPLICATES REMOVED)

L3 12926 S (CORRECTION FACTOR)

L4 19 S L3 AND (DNA) AND (GENE OR ARRAY OR CHIP OR ASSAY)

L5 15 DUP REM L4 (24 DUPLICATES REMOVED)

=> s L5 not L3

L6 15 L5 NOT L2

=> d L6 bib ab 1-15

L6 ANSWER 1 OF 15 BIOSIS COPYRIGHT 2001 BIOSIS

AN 2001:61263 BIOSIS

DM PREV200100061263

TI High-density microarray-mediated **gene** expression profiling of *Escherichia coli*.

AU Wei, Yan; Lee, Jian-Ming; Richmond, Craig; Blattner, Frederick R.; Rafalski, J. Antoni; LaRossa, Robert A. (1)

CF (1) Central Research and Development, Biochemical Science and Engineering, Experimental Station, DuPont Company, Wilmington, DE, 19380-0173; Robert.A.LaRossa@usa.dupont.com USA

SO Journal of Bacteriology, (January, 2001) Vol. 133, No. 1, pp. 545-556. print.

ISSN: 0021-9193.

DT Article

LA English

SL English

AB A nearly complete collection of 4,390 *Escherichia coli* open reading frames was amplified and arrayed in high density on glass slides. To exploit this reagent, conditions for RNA isolation from *E. coli* cells, cDNA production with attendant fluorescent dye incorporation, **DNA-DNA** hybridization, and hybrid quantitation have been established. A brief isopropyl-beta-D-thiogalactopyranoside (IPTG) treatment elevated *lacZ*, *lacY*, and *lacA* transcript content about 30-fold; in contrast, most other transcript titers remained unchanged. Distinct RNA expression patterns between *E. coli* cultures in the exponential and transitional phases of growth were catalogued, as were differences associated with culturing in minimal and rich media. The relative abundance of each transcript was estimated by using hybridization of a genomic **DNA**-derived, fluorescently labeled probe as a **correction factor**. This inventory provided a quantitative view of the steady-state level of each mRNA species. **Genes** the expression of which was detected by this method were enumerated, and results were compared with the current

LA ANSWER 2 OF 15 BIOSIS COPYRIGHT 2001 BIOSIS

AN 1009144230 BIOSIS

DN PREV199900442300

TI Ionizing radiation and genetic risks X. The potential "disease phenotypes" of radiation induced genetic damage in humans: Perspectives from human molecular biology and radiation genetics.

AU Sankaranarayanan, K. (1)

CS (1) Department of Radiation Genetics and Chemical Mutagenesis, Sylvius Laboratories, M&C, Leiden University Medical Centre, Wassenaarseweg 72, 2340 AB, Leiden Netherlands

SO Mutation Research, (Aug. 11, 1999) Vol. 419, No. 1, pp. 45-83.

ISSN: 0167-6369.

DT General Review

LA English

SL English

AB Estimates of genetic risks of radiation exposure of humans are traditionally expressed as expected increases in the frequencies of genetic disease (single-gene, chromosomal and multifactorial) over and above those of naturally-occurring ones in the population. An important assumption in expressing risks in this manner is that gonadal radiation exposures can cause an increase in the frequency of mutations and that this would result in an increase in the frequency of genetic diseases under study. However, despite compelling evidence for radiation induced mutations in experimental systems, no increases in the frequencies of genetic diseases of concern or other adverse effects (i.e., those which are not formally classified as genetic diseases), have been found in human studies involving parents who have sustained radiation exposures. The known differences between spontaneous mutations that underlie naturally-occurring single-gene diseases and radiation-induced mutations studied in experimental systems now permit us to address and resolve these issues to some extent. The fact that spontaneous mutations (among which are point mutations and DNA deletions generally restricted to the gene) originate through a number of different mechanisms and that the latter are intimately related to the DNA organization of the genes, are now well-documented. Further, spontaneous mutations include those that cause diseases through loss of function as well as gain of function of genes. In contrast, most radiation-induced mutations studied in experimental systems (although identified through the phenotypes of the marker genes) are predominantly multi-gene deletions which cause loss of function; the recoverability of an induced deletion in a livebirth seems dependent on whether the gene and the genomic region in which it is located can tolerate heterozygosity for the deletion and yet be compatible with viability. In retrospect, the successful mutation test systems (such as the mouse specific locus test) used in radiation studies have involved genes which are non-essential for survival and are also located in genomic regions, likewise non-essential for survival. In contrast, most of the human genes at which induced mutations have been looked for, do not seem to have these attributes. The inference therefore is that the failure to find induced germline mutations in humans is not due to the resistance of human genes to induced mutations but due to the structural and functional constraints associated with their recoverability in livebirths. Since the risk of inducible genetic diseases in humans is estimated using rates of "recovered" mutations in mice, there is a need to introduce appropriate correction factors to bridge the gap between these rates and the rates at which mutations causing diseases are potentially recoverable in humans. Since the whole genome is the "target" for radiation-induced genetic damage, the failure to find increases in the frequencies of specific single-gene diseases of societal concern does not imply that there are no genetic risks of radiation exposures: the problem lies in delineating the phenotypes of recoverable genetic damage that are recognizable in livebirths. Data from studies of naturally-occurring microdeletion syndromes in humans and those from mouse radiation studies are instructive in this regard. They (i) support the view that growth retardation, mental retardation and multisystem developmental abnormalities are likely to be among the quantitatively more important adverse effects of

radiation-induced genetic damage than mutations in a few selected genes and this underscores the need to expand the focus of risk estimation from known genetic diseases (as has been the case thus far) to include these induced adverse developmental effects although most of these are not formally classified as "genetic diseases". In absolute terms, however, the risk of adverse developmental effects (as extrapolated from mouse data) is still small and can be reconciled with the lack of demonstrable increases in untoward pregnancy outcomes in human studies (given the combination of radiation doses and sample sizes). Note that most of these adverse developmental effects are here assumed to be related to recoverable deletions or other gross changes induced in the genome and are predicted to show, by and large, autosomal dominant patterns of inheritance; their genetic basis, therefore, is not the same as that of many naturally-occurring congenital abnormalities which are interpreted as being multifactorial in origin.

LC ANSWER 3 OF 15 BIOSIS COPYRIGHT 2001 BIOSIS

AN 1998:910 BIOSIS

DN PREV19980000910

TI Preservation of blood and tissue samples for stable-carbon and stable-nitrogen isotope analysis.

AU Hobson, Keith A. (1) ; Gibbs, H. Lisle; Gloutney, Mark L.

CS (1) Canadian Wildlife Serv., 115 Perimeter Road, Saskatoon, SK S7N 0X4 Canada

SO Canadian Journal of Zoology, (Oct., 1997) Vol. 75, No. 10, pp. 1720-1723. ISSN: 0098-4391.

DT Article

LA English

SL English; French

AB Researchers engaged in collecting animal material for stable-carbon and stable-nitrogen isotope analysis are frequently faced with the need to preserve tissues prior to transportation to the laboratory. In many cases, freezing is not possible in the field, so we investigated the potential of several techniques for preserving tissues for this purpose. We also included preservation techniques used for DNA analyses in order to evaluate how they might alter delta13C and delta15N values in tissues and, ultimately, whether archived DNA samples could be used for stable-isotope **assay**. Tissues included blood and pectoral muscle from quail (*Coturnix coturnix japonica*) and blood from sheep (*Ovis aries*). Preservation techniques for blood included freeze-drying (control), drying on precombusted glass-fibre filter paper, and storing in 70% ethanol, 10% buffered formalin, ABL lysis buffer, and Queen's lysis buffer. After 8 weeks, the use of both lysis buffers and formalin resulted in significant depletion of 13C and 15N in blood. Values for samples dried on glass-fibre filter paper or stored in 70% ethanol did not differ significantly from those for the control. Muscle tissue was freeze-dried (control) or stored in 70% ethanol, 10% buffered formalin, or DMSO solution. Both the DMSO and formalin treatments resulted in significant depletion of 13C and 15N compared with the control. Only the 70% ethanol treatment did not result in changes to either isotope ratio in muscle. Where freezing is not possible, we recommend that blood samples be dried or stored in 70% ethanol. Our study provides an estimate of isotopic **correction factors** that may be applied to tissues archived for DNA analysis or stored in formalin.

LC ANSWER 4 OF 15 BIOSIS COPYRIGHT 2001 BIOSIS

AN 1997:67518 BIOSIS

DN PREV199700067518

TI Comparison of plasma virus loads among individuals infected with hepatitis C virus (HCV) genotypes 1, 2, and 3 by Quantiplex HCV RNA **assay** versions 1 and 2, Roche Monitor **assay**, and an in-house limiting dilution method.

AU Hawkins, A.; Davidson, F.; Simmonds, P. (1)

CS (1) Dep. Medical Microbiol., Univ. Edinburgh, Teviot Place, Edinburgh EH8 9AG UK

SO Journal of Clinical Microbiology, (1997) Vol. 35, No. 1, pp. 187-192. ISSN: 0095-1137.

DT Article

LA English

AB The accuracy of different methods for the quantitation of hepatitis C virus in plasma was measured with samples from individuals infected with different genotypes and by using RNA transcripts of predetermined concentrations. Highly reproducible results were observed upon repeat testing of samples by both the original version of the Chiron branched-DNA bDNA assay (Quantiplex RNA assay; bDNA-1) and the currently available version (Quantiplex HCV RNA 2.0 assay; bDNA 2.0). A greater variability was observed in the Roche Monitor assay (correlation coefficient of 0.537, compared with 0.943 and 0.984 for the bDNA-1 and bDNA-2 assays, respectively). Significant differences in the efficiency of detection of genotypes 1, 2, and 3 were observed for the bDNA-1 and Roche Monitor assays, whereas the bDNA-2 assay and nested PCR at limiting dilution were able to quantify genotypes with equal sensitivity. By quantifying RNA transcripts of different genotypes, the sensitivities of the Roche Monitor assay for sequences of the type 1 and type 3 transcripts were estimated to be 11 and 9, of those achieved for genotype 1. When **correction factors** based upon these results and those from quantitation of circulating viral RNA sequences in samples from blood donors were used, the genotypespecific differences in virus load in samples from blood donors were no longer observed, consistent with previous studies with corrected values from the bDNA-1 assay. These results suggest that many of the previous studies evaluating the effect of genotype and virus load in the response to interferon using methods such as the Roche Monitor assay and other competitive PCR methods require reinterpretation. Differences in efficiency of quantitation should be taken into account in future investigations of the relationship between genotype and virus load.

L6 ANSWER 5 OF 15 BIOSIS COPYRIGHT 2001 BIOSIS

AN 1996:423521 BIOSIS

IN EREV199698245677

TI In line monitoring of intracellular ATP concentration in Escherichia coli fermentations.

AU Lacks, Daniel R.; Wang, Daniel I. C. (1)

CS (1) Dep. Chemical Eng., Massachusetts Inst. Technol., Cambridge, MA 02139 USA

SO Biotechnology and Bioengineering, (1996) Vol. 52, No. 3, pp. 364-372.

ISSN: 1364-6592.

FT Article

LA English

AB A method was developed to provide a real-time measurement of intracellular adenosine 5'-triphosphate (ATP) concentrations in growing Escherichia coli. The bacteria to be monitored must first be modified by inserting the cDNA for firefly luciferase expressed from a constitutive promoter. Such a construct leads to constant specific activity of firefly luciferase during both the lag phase and exponential growth. When the luciferase substrate, D-luciferin, is added to the medium, ATP within the cells is utilized in the luciferase-catalyzed reaction that produces light. The light is carried from the bioreactor to a computer-based detector by an optical fiber. The detected per cell light emission varies during exponential growth. Analysis of cytoplasm extracts shows that this variance is related to changes in the ATP concentration, which ranges from 1 to 6 times the literature value for K-M. Experimental analyses demonstrated that inner filter effects are not a significant factor affecting the use of this system. The method was tested in a benchtop fermentor at cell densities above 13 g/L dry cell weight. A **correction factor** based on the accumulated light data is calculated and used in real time to account for consumption of luciferin from the culture broth by the light producing reaction. Dissolved oxygen concentrations must be kept above 15% of air saturation to ensure constant light output, but no detectable increase in oxygen demand is seen. The method does not significantly affect growth or production rates.

L6 ANSWER 6 OF 15 BIOSIS COPYRIGHT 2001 BIOSIS

AN 1994:497920 BIOSIS

IN EREV199497919820

TI Variance to mean ratio, R^2 , for poisson processes on phylogenetic trees.

AU Goldman, Nick

AS Lab. Mathematical Biol. National Inst. Med. Res., Ridgeley, Mill Hill
 London NW7 1AA UK
 SC Molecular Phylogenetics and Evolution, (1994) Vol. 9, No. 3, pp. 236-239.
 ISSN: 1055-7904.
 DT Article
 LA English
 AB The ratio of expected variance to mean, $R(t)$, of number of **DNA**
 base substitutions for contemporary sequences related by a "star"
 phylogeny is widely seen as a measure of the adherence of the sequences'
 evolution to a Poisson process with a molecular clock, as predicted by the
 "neutral theory" of molecular evolution under certain conditions. A number
 of estimators of $R(t)$ have been proposed, all predicted to have mean 1 and
 distributions based on the chi-2. Various **genes** have previously
 been analyzed and found to have values of $R(t)$ far in excess of 1, calling
 into question important aspects of the neutral theory. In this paper, I
 use Monte Carlo simulation to show that the previously suggested means and
 distributions of estimators of $R(t)$ are highly inaccurate. The analysis is
 applied to star phylogenies and to general phylogenetic trees, and
 well-known **gene** sequences are reanalyzed. For star phylogenies
 the results show that Kimura's estimators "The Neutral Theory of
 Molecular Evolution," Cambridge Univ. Press, Cambridge, 1983) are
 unsatisfactory for statistical testing of $R(t)$, but confirm the accuracy
 of Bulmer's **correction factor** (Genetics 123: 615-619,
 1979). For all three nonstar phylogenies studied, attained values of all
 three estimators of $R(t)$, although larger than 1, are within their true
 confidence limits under simple Poisson process models. This shows that
 lineage effects can be responsible for high estimates of $R(t)$, restoring
 some limited confidence in the molecular clock and showing that the
 distinction between lineage and molecular clock effects is vital. However,
 these results also indicate that $R(t)$ may be a poor statistic for
 analyzing the accuracy of Poisson process models and the molecular clock
 and that tests based on the whole likelihood function are more suitable.

L6 ANSWER 7 OF 15 BIOSIS COPYRIGHT 2011 BIOSIS

AN 1994:445746 BIOSIS

EN PREV184497184701

TI Enzymatic **assay** for quantification of deoxynucleoside
 triphosphates in human cells exposed to antiretroviral
 2',3'-dideoxynucleosides.

AU Gan, Wen-Yi (1); Johns, David S.; Mitsuya, Hiroaki

CS (1) Exp. Retroviral. Sect., Medicine Branch, Natl. Cancer Inst., Build.
 10, Room 5A24, Bethesda, MD 20892 USA

SO Analytical Biochemistry, 1994: Vol. 222, No. 1, pp. 110-122.
 ISSN: 0003-2697.

DT Article

LA English

AB Quantification of intracellular 2'-deoxynucleoside-5'-triphosphates (dNTPs)
 is of importance in studies of antiretroviral 2',3'-dideoxynucleoside
 analogs (ddNs) and a highly sensitive enzymatic **assay** for dNTPs
 has frequently been used for this purpose. However, the susceptibility of
 the **assay** to interference from the corresponding substrate
 analogs, ddNTPs, is still undefined. Ideally, **DNA** polymerases
 used in the **assay** should meet at least two criteria: (i) high
 fidelity to the template even in the presence of ddNTPs and (ii) low
 affinity for ddNTPs. None of the currently used exonuclease-free Klenow
 and Sequenase enzymes met both criteria. However, Sequenase had higher
 fidelity to the template than did the Klenow enzyme in the presence of
 pyrimidine-ddNTPs, and its reaction followed first order kinetics. We
 have, therefore relying primarily on Sequenase, designed a dNTP
 proportional reduction **assay** to correct the ddN-induced
 deviation in the enzymatic **assay**. With the use of high-fidelity
 exonucleasefree **DNA** polymerase and the application of
correction factors, we now can accurately quantify dNTPs
 with a minimum detection limit as low as 0.1 pmol, using as few as 1 times
 10⁴ peripheral blood mononuclear cells. The method described should be
 useful in the study and development of antiretroviral ddNs.

L6 ANSWER 8 OF 15 BIOSIS COPYRIGHT 2011 BIOSIS

AN 1994:44561 BIOSIS

IN PPEV128497:54251
 TI Fluorescence lifetime analysis of DNA intercalated ethidium bromide and quenching by free dye.
 AU Heller, Dennis P.; Greenstock, Clive L. (1)
 CS (1) Radiation Biol. Branch, AECL Res., Chalk River, ON K0J 1J0 Canada
 SO Biophysical Chemistry, (1984) Vol. 50, No. 2, pp. 305-312.
 IT Article
 LA English
 AB The fluorescence characteristics of ethidium bromide (Eb) complexed to calf thymus DNA have been examined using fluorescence lifetime analysis for a range of DNA (effective nucleotide concentration) to Eb molar ratios. Control of both temperature and ion concentration is necessary for reproducible analyses. Eb complexed to double stranded DNA has a maximum fluorescence lifetime of 13 ns and is easily distinguishable from a fluorescence lifetime value of 1.67 ns corresponding to unbound Eb. In a solution of calf thymus DNA containing excess Eb a binding equilibrium is reached, and this corresponds to one Eb molecule for every five nucleotides. With increasing amounts of unbound Eb, the fluorescence lifetime of the DNA-Eb complex decreases with a concomitant drop in the steady state fluorescence intensity, without a change in the amount of Eb bound to DNA. It is concluded that unbound Eb, acting via a quenching mechanism, shortens the fluorescence lifetime of bound Eb and consequently decreases the overall fluorescence intensity. This means that a different approach is necessary: time-resolved fluorescence spectroscopy directly distinguishes between a decrease in fluorescence intensity due to quenching by an excess of unbound Eb from that due to a decrease in Eb binding to double-stranded DNA. These studies suggest that techniques which measure total steady state fluorescence intensity of bound Eb in order to infer relative amounts of double-stranded DNA must be interpreted with caution. For such **assays** to be valid it is essential that no unbound Eb be present; otherwise a variable **correction factor** is required to account for unbound Eb.

L6 ANSWER 9 18 16 BIOSIS COPYRIGHT 2004 BIOSIS
 AN 1493:319686 BIOSIS
 IN PPEV128497:54251
 TI Optimum conditions for the **assay** of cardiac RNA: Comparative content and effect of hypertension.
 AU Siddiq, Tahar (1); Richardson, Peter T. (1); Preedy, Victor R.
 CS (1) Dep. Cardiol., King's Coll. Sch. Med., Dentistry, Bessemer Rd., London SE8 3PJ UK
 SO Biochemical Medicine and Metabolic Biology, (1993) Vol. 49, No. 2, pp. 148-163.
 ISSN: 0885-4509.
 IT Article
 LA English
 AB An investigation was made into techniques for the routine measurement of cardiac ribonucleic acid (RNA). Conditions were defined for the determination of rat ventricular RNA, based on uv absorption spectrophotometry. Optimum RNA hydrolysis occurred at 0.3 mol/liter alkali at 37 degree C for 1 h. Suitable **correction factors** for non-RNA material were also described and these gave similar results to RNA assayed by colorimetric methods. It was concluded that many of the methods previously reported may cause artifactual observations (in some cases apparent negative amounts of RNA). The technique was applied to the **assay** of RNA in various regions of the heart (i.e., left and right atrial and the left and right ventricular regions) and compared with noncardiac tissues (i.e., skeletal muscle, liver, bone, intestine, and kidney). The left ventricular RNA concentrations were comparable to the right ventricle and the interventricular septum, but approximately half that of atria. There were very little differences between left and right atrial regions. Differences between atrial and ventricular regions were reduced when data were expressed relative to DNA. The cardiac RNA content was shown to be comparable to skeletal muscle and bone. However, cardiac RNA concentrations were lower than those of kidney, liver, lung, and small intestine. Data were also expressed relative to DNA and showed that cardiac RNA/DNA ratios were higher than those of skeletal muscle and lower than those of bone, kidney, liver,

lung, and small intestine. The **assay** procedure for cardiac RNA was applied to investigations in the hypertrophied left ventricle induced by aortic constriction. After 10 days the RNA concentration (mg/g wet wt) and RNA content (mg/region) increased by 7 and 43, respectively.

LE ANSWER 10 OF 15 BIOSIS COPYRIGHT 2001 BIOSIS

AN 1987:110384 BIOSIS

IN BA-3:105014

TI INTERPRETATION OF THE LYMPHOID MODULATION IN THE FOLLICULAR CENTER A MORPHO-PHOTOMETRIC **ASSAY** OF STORED SLIDES STAINED WITH HEMATOXYLIN-EOSIN.

AU ESQUINAS J J; DEL MORAL P P

CS LOPEZ-CUERVO, SEFY. ANATOMIA PATOLOGICA. HOSP. "VIRGEN DE LAS NIEVES", GRANADA.

SC SANGRE (BARC), 1994 (RECD 1997) 31 (5), 521-533.

COEN: SNGRA. ISSN: 0034-4315.

FS BA; CML

LA Spanish

AB A photometric study of the different lymphoid cells comprised in the germinal centre was performed with a MPV2 Letiz photometer on stored slides from reactive lymph nodes, the nuclear size being also measured with a micrometric eyepiece. Original **correction factors** were introduced in order to homologate the measurements achieved. Different mean values were obtained ($p < 0.05$) when comparing the morphometric and photometric values of each cell type with the remaining ones. The smallest nuclear size corresponded to lymphocytes (4.67 microns) and the largest one was that of immunoblasts (9.63 microns). After arranging cell nuclei in accordance with their absorption, they were found to keep a sequence similar to that of the cell maturation pattern described by Lucas-Collins and Taylor. The values of nuclear extinction of small and large centrocytes (1.0 and 0.83) are one half that of the lymphocytes and immunoblasts (1.12 and 0.63, respectively). These findings that led us, in H-E stained slides, to identical interpretation of the morpho-functional lymphoid modulation than that attained through tritiated thymidine studies. Thus, data achieved by both methods allow us to assume that cleaved cells are in the S phase and contain amounts of **DNA** intermediate between that of the G1 cells (lymphocytes) and M phase cells (large centroblasts, immunoblasts).

LE ANSWER 11 OF 15 BIOSIS COPYRIGHT 2001 BIOSIS

AN 1986:224145 BIOSIS

DN BA81:119445

TI **CORRECTION FACTORS FOR THE DIPHENYLAMINE TEST FOR DNA IN YEASTS.**

AU SUBDEN R E; KRIDUS A

CS EXP. BOTANY GENETICS, UNIV. GUELPH, GUELPH, ONT. N1G 2W1, CAN.

SC MICROBIDS, 1985 (RECD 1990) 43 (1783), 213-244.

COEN: MICROB. ISSN: 0026-2683.

FS BA; DND

LA English

AB The diphenylamine **assay** for **DNA** content of yeast is unsatisfactory due to the presence of a yeast component which inhibits the colour reaction. The inhibitor is found in a wide range of yeast species and has not been identified. The relationships between the degree of inhibition and cell concentration, temperature and time of hydrolysis and extraction have been described. A formula for correction of the inhibition has been derived.

LE ANSWER 12 OF 15 BIOSIS COPYRIGHT 2001 BIOSIS

AN 1985:307621 BIOSIS

DN BA30:67613

TI SIGNIFICANCE OF SIMILARITIES IN PATTERNS AN APPLICATION TO BETA INTERFERON-RELATED **DNA** ON HUMAN CHROMOSOME 2.

AU MAY L T; LANDSBERGER F R; INDUYE M; SEHGAL P B

CS ROCKEFELLER UNIVERSITY, NEW YORK, N.Y. 10021.

SC PROC NATL ACAD SCI U S A, 1985 82 (12), 4193-4194.

COEN: PNASA. ISSN: 0027-8424.

FS BA; OLD

LA English

AB The nucleotide sequence of a 14-kilobase (kb) region of the human β -interferon (IFN- β) related DNA locus on chromosome (genomic DNA clone λ lambda.B3) was determined and compared to that of the IFN- β .1 gene by using the Sellers TT algorithm. This algorithm aligns segments of 1 sequence with similar segments in a 2nd sequence. A strategy was developed for assessing the significance of similarities between DNA sequences based on a scheme that recognizes patterns or runs of identities within an alignment. The pattern score (.PI.) thus obtained is an entropy-like measure. Numerically it is a reflection of the length of the 2nd longest run of identity in an alignment plus a **correction factor** due to the other shorter identity runs in the alignment. When the IFN- β .1 gene is compared to a random nucleotide sequence, the distribution of .PI. scores in such comparisons fits a Gaussian function. This strategy was used to identify 7 segments along the strand of λ lambda.B3 DNA that are related to segments in IFN- β .1; these 7 alignments have .PI. scores ≥ 1.9 standard deviations above the mean score obtained in comparisons between IFN- β .1 and random nucleotide sequences. One of these alignments (section 7) has a .PI. score 3.02 standard deviations above this mean score. The likelihood of finding an alignment statement as good as that in section 7 in a random sequence the length of the human genome is $\approx 10^{-7}$. The λ lambda.B3 DNA sequence in section 7 selects the human IFN- β .1 gene as the most significant alignment in computer searches of mammalian nucleotide sequence data bases.

LG ANSWER 13 OF 15 MEDLINE

AN 98494193 MEDLINE

DN 98494193

TI Accurate and absolute quantitative measurement of gene expression by single-tube RT-PCR and HPLC.

AU Hayward-Lester A; Gelfer P J; Sabatini S; Doris P A

CU Department of Cell Biology and Biochemistry, Texas Tech University Health Sciences Center, Lubbock 79430, USA.

NC DDBJ/SSB/ (NHGRI)

IFN1-HSG98201

DDK36113

SO GENOME RESEARCH, (1995 Dec 5 (4) 494-99.

Journal code: GES.

CY United States

DT Journal; Article; (JOURNAL ARTICLE)

LA English

ES Primary Journals

EM 1995

AB We report a method that allows accurate, absolute quantification of gene expression in a single reverse transcriptase (RT)-PCR reaction. This method makes use of novel high-performance liquid chromatography (HPLC) technology to resolve and quantify the products of competitive, mutant PNA PCRs. The HPLC technique allows rapid, high resolution of reaction products. On-line UV detection eliminates the need for radiolabel or other tracers. The HPLC technique also demonstrates that these competition reactions readily generate heteroduplex products. The ability of HPLC to resolve and quantify heteroduplex products is fundamental to the accuracy of the technique. Accurate measurements of gene expression have been obtained over four orders of magnitude and experiments employing predetermined quantities of specific native RNA input have demonstrated the ability of the system to provide absolute estimates of gene expression. Large size differences between native and mutant PNA inputs affected reverse transcriptase (RT) efficiency, but not PCR amplification efficiency. However, the magnitude of the RT efficiency effect can be estimated, is reproducible, and can therefore be adjusted by a calculated **correction factor**. The RT efficiency difference can be eliminated by reduction in the magnitude of the sequence difference between native and mutant PNA so that no **correction factor** is required. The application of the technique to quantification of expression of the alpha 1 subunit of sodium, potassium-ATPase in microdissected nephron segments is demonstrated.

LE ANSWER 14 OF 15 MEDLINE
 AN 85056916 MEDLINE
 DN 85056916
 TI Cell division does not affect Sendai virus genome replication in persistently infected BHK cells.
 AU Park L; Beffy P
 SO JOURNAL OF GENERAL VIROLOGY, (1984 Nov) 65 (Pt 11; 2855-60.
 JOURNAL CODE: JPR. ISSN: 0022-1317.
 CY ENGLAND: United Kingdom
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 ES Priority Journals; Cancer; Journals
 EM 1-8000
 AB The extent of Sendai virus genome replication in persistently infected BHK cells actively growing or at confluence was followed by estimation of the [3H]uridine incorporated into intracellular nucleocapsid RNA. First, we showed that, in the presence of actinomycin D, actively growing persistently infected cells were taking up threefold more [3H]uridine than resting cells. This higher uptake exhibited by growing cells was observed neither in persistently infected cells in the absence of actinomycin D, nor in acutely infected cells in the presence of actinomycin D. Assuming that the cellular pool of unlabelled uridine stays constant, we used a **correction factor** for this difference in [3H]uridine uptake and estimated [3H]uridine incorporation in nucleocapsid RNA, normalising the data either to the amount of cell or of viral template. Results showed that the viral genome replication, expressed either way, was not significantly influenced by cell growth conditions.

281.56

LE ANSWER 15 OF 15 SCISEARCH COPYRIGHT 1991 ISI (P)
 AN 85071923 SCISEARCH
 GA The Genuine Article (P) Number: UK963
 TI DOSE-RESPONSE CURVES FOR SIMPLE AND COMPLEX CHROMOSOME-ABERRATIONS INDUCED BY X-RAYS AND DETECTED USING FLUORESCENCE IN-SITU HYBRIDIZATION
 AU SIMSON P J (Reprint); SAVAGE J R K
 SO IIRC, RADIAT & GENOME STABIL UNIT, CHROMOSOME DAMAGE GRP, HARWELL IX11 ORD, BEERKS, ENGLAND (Reprint)
 CYA ENGLAND
 SO INTERNATIONAL JOURNAL OF RADIATION BIOLOGY, (APR 1986) Vol. 69, No. 4, pp. 429-446.
 ISSN: 0955-3002.
 DT Article; Journal
 ES LIFE
 LA ENGLISH
 REC Reference Count: 21
 ABSTRACT IS AVAILABLE IN THE ALL ANI IALL FORMATS
 AB A primary human fibroblast cell-line was grown to confluence and X-irradiated at 2, 4 and 6 Gy. The resulting chromosome aberrations were detected in first-division cells using a series of FISH **assays** in which either one or two chromosomes (nos. 1, 2, 4, 5, 7 and 13) and all centromeres were painted with distinct colours. Interchange aberrations were classed as simples if they appeared to originate from a break in each of two chromosomes (dicentric with fragment or reciprocal translocation), or complexes if their origins required three or more breaks in two or more chromosomes. Breaks not obviously connected with exchanges were also scored. The data were corrected to include paint patterns resulting from either incomplete or terminal exchanges. In addition we attempted to correct for the apparently simple exchanges which are actually derived from complex interactions (pseudosimples) using **correction factors** calculated by establishing the predominant complex families present at each dose. Power Law analysis of the corrected data showed a linear dose-response for simple exchanges and a dose-squared response for complex exchanges. Based this observation we suggest that simples result lesions induced by the same radiation track and complexes arise from the interaction of lesions induced by separate tracks.

FILE 'HOME' ENTERED AT 16:19:54 ON 01 FEB 2001

FILE 'BIOSIS, CAPLUS, MEDLINE, SCISEARCH' ENTERED AT 16:19:14 ON 01 FEB 2001

L1 38 S (FILTER OR ARTIFACT OR ANOMAL?) AND ((GENE ARRAY) OR *GENE CH
L2 17 DUP REM L1 (21 DUPLICATES REMOVED)
L3 12926 S (CORRECTION FACTOR)
L4 39 S L3 AND (DNA) AND (GENE OR ARRAY OR CHIP OR ASSAY)
L5 15 DUP REM L4 (24 DUPLICATES REMOVED)
L6 15 S L5 NOT L2